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n.a. database search, using Smith-Waterman algorithm n.a. ch_nn

MasPar time 1134.44 Seconds 1365.449 Million cell updates/sec Tue Dec 15 18:30:42 1998; Run on:

Tabular output not generated.

>US-09-109-864-1 (1-865) from US09109864.seq 865 Description: Perfect Score:

N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

2275025 seqs, 895388244 bases x 2 Searched:

Minimum Match 0% Listing first 45 Post-processing:

summaries

emb1-est55

Database:

5:9b_est1 6:9b_est10 7:9b_est11 8:9b_est12 9:9b_est13 10:9b_est14 11:9b_est15 12:9b_est16 13:9b_est17 14:9b_est18 15:9b_est2 17:9b_est2 17:9b_est20 18:9b_est2 17:9b_est2 17:9b_est20 18:9b_est2 17:9b_est5 22:9b_est6 23:9b_est2 24:9b_est8 25:9b_est9 26:9b_qss1 27:9b_gss2 28:9b_gss3 29:9b_gss4 1:em_estl 2:em_gssl 3:em_gss2 4:em_gss3 genbank-estl07 Database:

Mean 12.059: Variance 7.331; scale 1.645 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

2.06e-287 2.64e-199 1.44e-120 2.17e-53 2.17e-28 9.89e-17 2.79e-13 1.77e-10 6.32e-10 6.32e-10 Pred. No. EST181872 Jurkat T-cel y059h05; rl Homo sapien y059h05; al Homo sapien EST5588 Infant adrena ze63all.rl Soares reti 975N178? Rice Immature yh96al2.rl Homo sapien Dictyostelium discoide qq33f09.xl Soares_preg 978N1784 Rice Immature Dictyostelium discoide Description H30148 H27468 AA349100 AA020729 AA001029 AA754459 R37188 C84867 A1128239 AA754458 C24325 AA311108 H Query Match Length DB Score Result No. 312119 Û

Bioinformatics The Institute for Genomic Research

Other_ESTs: THC124424 Contact: Kerlavage, AR

JOURNAL MEDEINE COMMENT

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ALIGNMENTS

AA311108 496 bp mRNA EST 19-APR-1997 EST181872 Jurkat T-cells V Homo sapiens CDNA 5' end, mRNA sequence. 4A311108 91963435 EST. human. human Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Filzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kalley, J.C., Liu, LI., Marmarcs, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Bednarik, D.D., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y., Bednarik, D.D., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Mudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Medisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,	<pre>Fraser,C.W. and Venter,J.C. Initial assessment of human gene diversity and expression patterns</pre>	Dased upon 81 million nucleatides of club sequence Nature 377 (6547 suppl), 3-174 (1995)
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                                        For clone availability, additional sequence and expression information related to this EST, please check the TiGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
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Pred. No. 2.06e-287;
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/db_xref="taxon:9606"
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot - 20. Library constructed by Bento Soares
                                                                                                                                                                                Eukaryotae; Metazoa, Eumetazoa; Bilateria; Coelomata; Deukaryotae; Metazoa, Eurebrata; Gnathostomata; Osteichthyes; Sarcoptersygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 411)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
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/clone="182265"
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                              and M.Fatima Bonaldo.
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Best Local Similarity 95.7%;
Matches 360; Conservative
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WashU-Merck EST Pr
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 15 15:55:11 1998; MasPar time 5.67 Seconds 629.394 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-109-864-2 (1-133) from US09109864.pep 980 1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

74019 seqs, 26840295 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot35 1:swissprot Database:

Mean 44.065: Variance 78.778; scale 0.559 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. N	2.71e-14	2.88e-09	3.11e-08	3.11e-08	1.49e-07	9.88e-06	1.12e-03	1.12e-03	3.21e-03	3.21e-03	9.03e-03	9.41e-02	1.30e-01	1.80e-01	3.42e-0]	4.70e-0]	6.43e-01	6.43e-01	8.79e-01	8.79e-0]	8.79e-0	1.63e+00	1.63e+00
Description	GALECTIN-5 (RL-18).	GALECTIN-9 (36 KD BETA	GALECTIN-8 (PROSTATE C	GALECTIN-9.	GALECTIN-7 (HKL-14).	GALECTIN-9 (HOM-HD-21)	32 KD BETA-GALACTOSIDE	PROBABLE 33 KD BETA-GA	GALECTIN-8 (30 KD S-TY	GALECTIN-4 (LACTOSE-BI	UDP-N-ACETYLGLUCOSAMIN	BETA-GALACTOSIDE-BINDI	COPPER TRANSPORT ATP-B	HYPOTHETICAL 21.0 KD P	FERRIC ENTEROBACTIN RE	GALECTIN-7.	PROBABLE GENERAL SECRE	SODIUM CMANNEL PROTETN	PREPROTEIN TRANSLOCASE	COMPLEMENT FACTOR I PR	GLUTATHIONE-REGULATED	MULTIDRUG RESISTANCE P	COENZYME POQ SYNTHESIS
А	LEG5_RAT	LEG9_RAT	LEG8_HUMAN	LEG9_MOUSE	LEG7_HUMAN	LEG9_HUMAN	LE32_CAEEL	LE33_CAEEL	LEG8_RAT	LEG4_RAT	GPT_YEAST	LEG4_CHICK	NOSF_PSEST	YRNA_CAEEL	PFEA PSEAE	LEG7_RAT	GSPE_ECOLI	CINI_LOLBL	SECY STRGR	CFAI_HUMAN	KEFC_ECOLI	EMRB_HAEIN	POOF_KLEPN
g :	-	-	-	-	H	Н	-	-	Η	-	-	-	-	-	Н	-	Н	-	-	-	-	-	-
Length DB	144	354	316	353	135	322	279	289	316	324	448	134	308	184	746	135	493	1522	437	583	620	510	761
& Query Match	17.8	14.9	14.3	14.3	13.9	12.8	11.4	11.4	11.1	11.1	10.8	10.1	10.0	6.	9.7	9.6	9.5	6	4.6	9.4	4.6	9.5	9.5
Score	174	146	140	140	136	125	112	112	109	109	106	66	86	97	95	94	93	93	92	92	92	90	90
Result No.	1	7	m	4	S	9	7	ω	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23

: | ::| :|| 117 LRELRISGSVQL 128 128 INTLEVAGDIQL 139

g . Ω

2.21e+00 2.21e+00 2.21e+00 2.29e+00 2.98e+00 4.02e+00 4.0	E	Gaps 6; vvr 68 : : : LAW 62 LPD 127 : :
GLOBAL NITROGEN REGULA GALECTIN-4 (LACTOSE-BI HYPOTHETICAL PROTEIN C FIBER PROTEIN. PUTATIVE YOP PROTEINS SULFITE REDUCTASE, ASS COAT PROTEIN (CAPSID P SEPLAPTERIN REDUCTASE DNA POLYMERASE III, DE HYPOTHETICAL 86.8 KD P DNA-DIRECTED RNA POLYM ENDOGLUCANASE P RECUR HYDROXYATRAZINE HYDROL GLOBAL NITROGEN REGULA GALECTIN-3 (GALACTOSE- MODIFICATION METHYLASE NEURONAL ACETYLCHOLINE ENDOGLUCANASE G PRECUR MRNA CAPPING ENZYME (M ENDOGLUCANASE G PRECUR MRNA CAPPING ENZYME (M ENDOGLUCANASE I (ENDOGLUC	STANDARD; PRT; 144 AA. 96 (REL. 33, CREATED) 966 (REL. 33, LAST SEQUENCE UPDATE) 966 (REL. 33, LAST ANNOTATION UPDATE) 5 (RL-18). 1. METAZOA; CHORDATA; VERTEBRATA; TETRAPODA: MAMMALIA; RODENTIA. RODENTIA. FROM N.A., AND PARTIAL SEQUENCE. 971504072755; 97157487. 1700. MACER M.F., LEFFLER H., HERRMANN J., XIA YR., CONDER D.N.W. LIGHTS A.J.—BARONDES S.H.; CHON MAY TOUCTION IN EXTHROCYTE DIFFERENTIATION. 11 MONOMER. 11 MONOMER. 12 MONOMER. 13 ACETYLATION. 14 AA: 16065 MW; 5C7CC533 CRC32: 144 AA: 16065 MW; 5C7CC533 CRC32: 144 AA: 16065 MW; 5C7CC533 CRC32:	tch 17.8%: Score 174; DB 1: Length 144; al Similarity 28.0%: Pred. No. 2.71e-14: 37: Conservative 38: Mismatches 49; Indels 8; Ga; PNLAVPFFTSIPNGLYPSKSIVISGVVLSDAKRFQINLRC-GGDIAFHLNPRFDENAVVR
NTCA_SYNY3 LEG4_HUMAN FIEG4_HUMAN FIEGA_CHPO SCE_YEREN SIR_DESYH COAT_ESWH SPRE_RAT HOLA_ECOLI YBIO_ECOLI TAIO_ECOLI RPOD_MAIZE GUNA_CALSA ATZB_PEESCH NTCA_ANASP ILEG3_CRILO MTCA_ANASP NTCA_ANASP NTCA_ANASP NTCA_ANASP NTCA_ANASP MTCA_ANASP MTCA_ANASP GUNG_CLICCE MCE_ASFR7 GUNG_CLICCE MCE_ASFR7 GUNG_CLICCE MCE_ASFR7 GUNG_CLICCE MCE_ASFR7 GUNG_CLICCE MCE_ASFR7 GUNG_CLICCE MCE_ASFR7	FRATED) AST SEQUENCE UPDATE) AST ANNOTATION UPDATE AST ANNOTATION UPDATE FRATIAL SEQUENCE. LEFFLER H., HERRMANN W. LIGHTS AND TO THE PARTHECYTE D TON IN ERYTHECYTE D ERYTHECYTE D TO THE GALAPTIN (S LATION. ACETILATION. BETA-GALACTOSI GENW: SC7CC533 CRC	Score 174; Pred. No. 38: Misma /ISGVVLSDAKR! :: : : : SRGQRF-SVMILL
225 323 323 1 976 1137 1137 1158 1152 1152 1152 1152 1152 1152 1162 1174	STANDARD; L. 33, CREATED) L. 33, LAST SEG L. 33, LAST SEG L. 33, LAST ANN 18). US (RAT). ZOA: CHORDATA; TIA. A. AND PARTIA CTTES; R M.F., LEFFLER TYTORIC TO THE PELONGS TO THE TECTIN CALAC 727176	tch al Similarity 28 0%: Pred 37: Conservative 38: PNLAVPFFTSIPNGLYPSKSIVISGVV
00000000000000000000000000000000000000	15_RAT STANDARD; 967: FEB-1996 (REL. 33, LAR FEB-1996 (REL. 33, LAR FEB-1996 (REL. 33, LAR LECTIN-5 (RL-18). LLS5.	imilarity 7: Conse: WPFFTSIPW 11 :: WPCSHALPQ NNSWGPEER: NNSWGPEER: SR-WG-QKK:
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 FEBS-RAT 1-FEB-19 1	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
ପର୍ଗ୍ରୀ ପ୍ରେଲ୍ଲ୍ଲ୍ଲ୍ଲ୍ଲ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ୍କ	STTTTT SO S S S S S S S S S S S S S S S	Query Best 1 Matche Db CQY OQY OQY

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EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96293510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQDENCE FROM N.A.
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MEDLINE; 97298141
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSDE-PROSTATE;
LEGB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALECTIN-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEG9_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                           REAR ROCCORDED DE PERCENTAL DE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABRAMSON R.G.;

J. BIOL. CHEM. 272:617-625(1997)

-1-FUNCTION: BINDS GALACTOSIDES MAY PLAY A ROLE IN THYMOCYTE-
FUNCTION: BINDS GALACTOSIDES RELEVANT TO TRE BIOLOGY OF THE THYMUS (BY
SIMILARITY). MAY PROVIDE THE MOLECULAR BASIS FOR URATE FLUX ACROSS
CELL MEMBRANES, ALLOWING URATE THAT IS FORMED DORING PORINE
METABOLISM TO EFFLUX FROM CELLS AND SERVING AS AN ELECTROGENIC
TRANSPORTER THAT PLAYS AN IMPORTANT ROLE IN RENAL AND
GASTROINTESTINAL URATE EXCRETION. HIGHLY SELECTIVE TO THE ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSICAL SECRETORY PATHWAY (BY SIMILARITY).
--- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED BY
ALTERNATIVE SPLICING. THE LONG FORM (SHOWN HERE) IS EXPRESSED
EXCLOSIVELY IN THE SMALL INTESTINE.
--- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 RNTQINNSWGPEERSLPGRMPFNRGQSFSVWILCEGHCFKVAVDGQHICEYYHRLKNLPD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 TPAYTIPFFTSIPNGFYPSKSINISGVVLPDAKRFHINLRC-GGDIAFHLNPRFNEKVVV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (SHORT FORM).
STRAIN-SPRAGDE-DAWLEY; TISSUE-KIDNEY;
LEAL-PINTO E., TAO W., RAPPAPORT J., RICHARDSON M., KNORR B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILAKILI.
EMBL: U59462; G1916610; -.
EMBL: U72741; -; NOT_ANNOTATED_CDS.
EMBL: D67958; G1864095; -.
PROSITE; PS00309; LECTIN. CALACTOSIDE; 2.
GALAPTIN; LECTIN; REPEAT; ALTENATIVE SPLICING; ION TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
BISSING (IN SHORT ISOFORM).
L -> M (IN REF. 2).
CTEB7FEA CRC32;
                                                                                                                                                                                                                                                                                                                                           LGALSY.
RATUDS NORVEGICUS (RAI).
EDKARYOTA METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHBRIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 146; DB 1; Length 354; Pred. No. 2.88e-09;
                                                                                                                               P97840; 008588;
01-NOY-1997 (REL. 35, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANDTAVION UPDATE)
GALECTIN-9 (36 KD BETA-GALACTOSIDE BINDING LECTIN) (URATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY, AND SMALL INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAINS.
-!- SIMILARITY: BELONGS TO TRE GALAPTIN (S-LECTIN) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
                                                                                                           354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (LONG AND SHORT FORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALAPTIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WADA J., KANWAR Y.S.;
J. BIOL. CHEM. 272:6078-6086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39946 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%;
ilarity 23.4%;
Conservative
                                                                                                                                                                                                                                                                                                            TRANSPORTER/CHANNEL) (DAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | ::| :|| |::
117 LRELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 INTLEVAGDIQLIHVOT 354
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
286 2
148 1
187 1
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE, 97190351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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VARSPLIC
CONFLICT
SEQDENCE
                                                                                                       LEG9_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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FROC. NATL. ACAD. SCI. U.S.A. 93:7252-7257(1996).

1. SUBCELIDITAR LOCATION: CTTOPLASMIC (PROBABLE).

1. SUBCELIDITAR LOCATION: CTTOPLASMIC (PROBABLE).

1. TISSUE SPECIFFORTY: SELECTIVE EXPRESSION BY PROSTATE CARCINOMAS VERSUS NORMAL PROSTATE AND BENIGN PROSTATIC HYBERTROPHY.

1. DOMAIN: CONTAINS TWO HOMOLOCODS BUT DISTINCT CARBOHYDRATE-BINDING DOMAINS.

1. SIMILARITY: BELONGS TO TWE GALAPTIN (S-LECTIN) FAMILY.

FRABL: 78132: 1213.

GALACTIN; REPEAT: ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 TPQLSLPFAARLNTPMGPGRTVVVQGEVNANAKSFNVDLLAGKSKDIALHLNPRLNIKAF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 VRNSFLQESWGEEERMITSFPFSPGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKE-LS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADA J., OTA K., KUMAR A., WALLNER E.I., KANWAR Y.S.;
J. CLIN. INVEST. 99:2452-2461(1997).
-i- FUNCTION: BINDS GALACTORES. MAY PLAY A ROLE IN THYMOCYTE-
EPITHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                         EDKARYOTA; METAZOA; CRORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY)
EB4D9A3D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEDEBNCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECTIN-8 (PROSTATE CARCINOMA TUMOR ANTIGEN) (PCTA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 140; DB 1; Le
Pred. No. 3.11e-08;
41; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CD-1; TISSUE-SMALL INTESTINE, AND KIDNEY;
MEDLINE; 97190351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   006573; 008572;
01-NOV-1997 (REL. 35, CREATED)
10-NOV-1997 (REL. 35, LAST SEQDENCE UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 AA
316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALAPTIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WADA J., KANWAR Y.S.;
J. BIOL. CMEM. 272:6078-6086(1997).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | |:| ::| |:|
116 QLRELRISGSVQLYCVMS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 SIDTLEINGDIMLLEVRS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 24.6%;
34; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315
254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCDLDS (MOUSE)
                                                                                                                                  HOMO SAPIENS (HUMAN)
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185 3
248 2
316 AA;
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GALECTIN-9 (HOM-HD-21).
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206
355
355
180
180
135
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                                                                                                      MIM; 600615; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; F
GALAPTIN;
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                             INIT_MET
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                               Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIAMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGALS9
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E SOLIA SOLI
    SSEER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGNALDO T., BERNERD F., DARMON M.;
SUBMITTED (XXX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: COULD BE INVOLVED IN CELL-CELL AND/OR CELL-MAIRIX
INTERACTIONS NECESSARY FOR NORWAL GROWTH CONTROL.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: MAY BE SECRETED BY A NON-CLASSICAL SECRETORY
                                  -:- IISSUE SPECIFICITY: ACCEMPATED EXPRESSION IN LIVER AND THYMUS OF EMBRYO, DETECTED IN EMBRYONIC HEART, BRAIN, LUNG, LIVER, AND KIDNEY, HIGHLY EXPRESSED IN ADUCT INVEME, SMALL INTESTINE, AND LIVER, AND TO A LESSER EXTENT IN LUNG, KIDNEY, SPLEEN, CARDIAC, AND SKELETAL MUSCLE. BARELY DETECTABLE IN BRAIN AND RETICULOCYTE.
-:- DEVELOPMENTAL STAGE: THE EXPRESSION INCREASED WITH SUCCESSIVE STAGES OF EMBRYONIC DEVELOPMENT.
-:- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM (SNOWN HERE) IS EXPRESSED EXCLUSIVELLY IN THE SMALL INTESTINE.
-:- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADSEN P., RASMUSSEN H.H., FLINT T., GROMOV P., KRUSE T.A., HONORE B., VORUM H., CELIS J.E.:
J. BIOL. CHEM. 270:5823-5829(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 RNTQINNSWGQEERSLLGRMPFSRGQSFSVWIICEGHCFKVAVNGQHMCEYYHRLKNLQD 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 TPAYTIPFYTPIPNGLYPSKSIMISGNVLPDATRFHINLRC-GGDIAFHLNPRFNENAVY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 W---ISR-WGOK-KLISAPFLFYPORFFEVLLFOEGGLKLALNGOGLGATSMNOOALEO 116
    SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 7-19; 75-82; 111-117 AND 120-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SNORI ISOFORM).
1AC8AD75 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 353;
                                                                                                                                                                                                                                                                             -:- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 140; DB 1; I
Pred. No. 3.11e-08;
40; Mismatches 58;
                                                                                                                                                                                                                                                                                              EMBL; U55061; G1916604; -...
EMBL; U55060; G1916602; -...
MGD; MG1:109496; LGALSO
PROSITE; PS00309; LECTIN_GALACTOSIDE; 2...
GALAPIN; LECTIN; REPEAT; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JT 5
LEG7_HUMAN STANDARD; PRT; 135 AA.
P47929.9
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
GALECIN-7 (HKL-14).
                                                                                                                                                                                                                                                                                                                                                                                                    GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         GALAPTIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER
                    CLASSICAL SECRETORY PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40036 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%;
ilarity 24.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | ::| :|| |::
117 LRELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 INTLEVAGDIOLTHVOT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                       353
87
291
178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285
148
353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
hes 33; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-EPIDERMIS;
MEDLINE; 95197604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-EPIDERMIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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Matches
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-:- FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
EPITHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS.
-:- TISSUE SPECIFICITY: PERIPHERAL BIOD LEUKOCYTES AND LYMPHATIC
TISSUES. OVEREXPRESSED IN HODGKIN'S DISEASE TISSUE.
-:- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NSKEQGSWGREERGPGVPFOR-GOPF-EVLIIASDDGFK-AVVGDAQYNHFRNRLPLARV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVF 61
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
-i- TISSUE SPECIFICITY: MAINLY IN STRATIFIED SQUAMOUS EPITHELIUM.
-i- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINKER.
GALAPTIN 2.
GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARIIY).
BETA-GALACTOSIDE (BY SIMILARIIY).
MISSING (IN SHORT ISOFORM).
K -> R (IN REF. 1).
S -> F (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (NUMAN).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-SPLEEN;
MEDLINE; 91197815.
TUBERCI O., SCHALTT H., FADLE N., PFREUNDSCHUH M., SAHIN U.,
J. BIOL. CNEM. 272:6416-6422(1997).
                                                                                                                                                                                                                                                                                                                                               13.9%; Score 136; DB 1; Length 135; 28.1%; Pred. No. 1.49e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED ALIERNATIVE SPLICING.
-1- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
EMBL: Z49107: B310691: -.
                                                                                                                                                                                                                                                               BETA-GALACTOSIDE (POTENTIAL).
33656F93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          39; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITIED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LECTIN_GALACTOSIDE; 2.
REPEAT; ALTERNATIVE SPLICING.
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEG9_HUMAN STANDARD; PRT; 355 AA. 000182; 014532; CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST SANOTATION UPDATE)
                                                                                                                                                                      PROSITE; PS00309; LECTIN_GALACTOSIDE; 1. GALAPTIN; LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (LONG FORM).
TISSUE-GASTRIC CARCINOMA;
KATO S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (SHORT FORM)
                                                                                                                                                                                                                                                                                          135 AA; 14944 MW;
                                                     EMBL; L07769; G182132; --
EMBL; U06643; G458703; --
AARRUS/GHENT-2DPAGE; 17; IEF.
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 28.1%;
hes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z49107; E310691; -. EMBL; AB006782; D1023026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 RLVEVGGDVOLDSVR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : ::| ||| |:
118 RELRISGSVQLYCVH 132
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01-OCT-1996 (REL. 34, CREATED)
1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDTAILON UPDATE)
PROBABLE 33 XD BETA-GALACTOSIDE-BINDING LECTIN (33 KD GBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGALS8
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      SO FIT WAS COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN THE CO
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                                                                                                                                                                                                                                                234 GLYPSKSILLSGTVLPSAQRFHINLCS-GNHIAFHLNPRFDENAVVRNTQIDNSWGSEER 292
                                                                                                                                                                                                                                                                                                                                                                     293 SLPRKMPFVRGOSFSVWILCEANCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTH 352
                                                                                                                                                                                                                                                                                                                                                                                                        16 GLSPGQVIIVRGLVLQEPKHFTVSLRDQAAHAPVTLRASFADRTLAW---I-SRWG-QKK 70
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RRABDITIDA
                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 BETA-GALACTOSIDE (BY SIMILARITY) 31809 MW; D6BA48DB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                        Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: BINDS GALACTOSE.
-i- PTM: THE N-TERMINAL IS BLOCKED.
-i- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
EMBL: M94671; G156210; -.
EMBL: ABOOG 02: D1023816; -.
PIR: S27798; S27798.
PIR: S27798.
PIR: A42846; A42846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 279;
                                                                                                                     Score 125; DB 1; Length 355
Fred. No. 9.88e-06;
32; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
32 KD BETA-GALACTOSIDE-BINDING LECTIH (32 KD GBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIRABAYASBI J., SATOH H., OHYAMA Y., KASAI K.-I.,
J. BIOCHEM. 111:553-555(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 112; DB 1; Le
Pred. No. 1.12e-03;
12; Mismatches 13;
P -> L (IN REF. 1).
E -> G (IN REF. 1).
: 2EOD41C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VPYRSVLOEKFEPGQTLIVKGSTIDESQRFTINLHSKTA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALAPTIN 1.
GALAPTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00309; LECTIN_GALACTOSIDE; 2. GALAPTIN; LECTIH; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92348399.
HIRABAYASHI J., SATOH M., KASAI K.-I.;
J. BIOL. CHEM. 267:15485-15490(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97476274.
ARAIA Y., HIRABAYASHI J., KASAI K.-I.;
J. BIOL. CHEM. 272:26669-26677(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
270 270 P
313 313 E
355 AA; 39518 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 35.9%;
Matches 14; Conservative
                                                                                                                     Match 12.8%;
Local Similarity 25.2%;
es 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 202-220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92348337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 VQT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::
131 VHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE32_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
BINDING
SEQUENCE
   COHFLICT
                                                            SEQUENCE
                                                                                                                        Query Match
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Matches
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289 AA

PRT:

STANDARD;

LE33_CAEEL Q09581;

RESULT ID LE AC 00

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-1- DEVELOPMENTAL STAGE: VERY LOW LEVELS IN WHOLE EMBRYOS, HIGH LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95155445.
HADARI Y.R., PAZ K., DEKEL R., MESTROVIC T., ACCILI D., ZICK Y.;
HADARI Y.R., PAZ K., DEKEL R., MESTROVIC T., ACCILI D., ZICK Y.;
J. BIOL. CHEM. 270:3447-3453(1995).
-!- FUNCTIOH: POSSESS SUGAR BINDING AND HEMAGGLUTINATION ACTIVITY.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 HLSLPFEARLNASMGPGRTVVVKGEVNTNATSFNVDLVAGRSRDIALHLNPRLNVKAFVR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RLEVPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSL-RDQAAHAPVTLRASFADRTLAW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                              EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, CARDIAC MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RATTUS HORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY)
96341BC7 CRC32;
                                                                                                                                                                               -: FUNCTION: BINDS GALACTOSE (BY SIMILARITY).
-: SIHILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY
EMBL: ZR8636, 1750605,
WORNPEP: XR892.1: CE01724,
PROSITE; PS00309; LECTIN GALACTOSIDE; 1.
DOMAIN 142 289
GALAPTIN 1.
DOMAIN 142 289
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN ADULT TISSUES.
-!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY EMBL; 09824; G717032; -. PROSITE: PSO0309; LECTIN, GALACTOSIDE; 1. GALAPTIN; LECTIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109; DB 1; Length 316
Pred. Ho. 3.21e-03;
41; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 112; DB 1; Length 289
Pred. Ho. 1.12e-03;
17; Mismatches 12; Indels
                                                                                         SECUENCE FROM N.A.
STRAIN-BRISTOL N2;
LLOYD C.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LEVPCSHALPQGLSPGQVIIVRGLVLOEPKHFTVSLRDQAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 IHIPYRSKLTERIEPGQTLIIRGKTIDESKRFNINLHKDSP 51
                                                                                                                                                                                                                                                                                                                                                      142 289 GALAPTIN 2.
289 AA; 32991 MW; 3329858D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-HOV-1997 (REL. 35, CREATED)
01-HOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECTIN-8 (30 KD S-TYPE LECTIN) (RL-30).
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LINKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 316 G
248 254 B
316 AA; 36038 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%;
[larity 22.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Hatch 11.4%;
Best Local Similarity 29.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
ZK892.1.
CAENORHABDITIS ELEGAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Hatch
Best Local Similarity 2
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                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 9
LEGB_RAT
Q62665;
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BINDING
SEQUENCE
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-i- ILSUB SPECIFICITY: HIGHLY EXPRESSED IN FULL-LENGTB FORM IN SMALL AND LANGE INTESTIES AND STOMACH BUT WAS NOT DETECTED IN OTHER TISSUES INCLUDING LUNG, LIVER, KIDNEY, AND SPLEEN.
-i- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                       | : ||: ||: || : || : ||: ||: || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 VPYVGTLQGGLTARRIIIIKGYVLPTAKNLIINFKVGSTGDIAFHMNPRIGDCVVRNSYM 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 NGSWGSEE-RKIPYNPFGAGOFFDLSIRCGTDRFKVFANGOHLFDFSHRFQAFQRVDMLE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 NSFLQDAWGEEERNITCFPFSSGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKD-LSSI 299
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01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
15-UTL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-INTESTINE;
MEDLINE; 93194902.
ODA Y., HERRANN J., GITT M., TURCK C.W., BURLINGAME A.L.,
BARONDES S.H., LEFFLER H.,
J. BIOL. CHEM. 268:5929-5939(1993).
I. BIOL. CHEM. 268:5929-5939(1993).
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01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LEST ANNOTATION UPDATE)
UPDAT-1996 (REL. 34, LEST ANNOTATION UPDATE)
UPD-N-ACETIKGLUGOSAMINE--DOLICHYL-PHOSPBATE N-
ACETIKGLUGOSAMINEPHOSPHOTRANSFERASE (EC 2.7.8.15) (GPT) (GIPT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY).
9870240B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 109; DB 1; Length 324;
Pred. No. 3.21e-03;
38; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELQNGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                            324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00309; LECTIN_GALACTOSIDE; 2. GALAPTIN; LECTIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                              PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.1%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: M73553; G294572; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Conservative
                                                                                                                                       300 DTLAVDGDIRLLDVRS 315
                                                                                                                                                                                            118 RELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIANDARD;
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : | |:
ISGSVOLYCVH 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
257
324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A46631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A46631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAINS.
                                                                                                                                                                                                                                                          10
LEG4_RAT
P38552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CT 11
GPT_YEAST
P07286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (L36LBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DORAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                    윰
                                                                                                                                                                                                                                                                                                                                                                                           THE SOUND AND A SECOND AS A SE
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01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
BETA-CALACTOSIDE-BINDING LECTIN (14 KD LECTIN) (C-14).
GALLUS GALLUS (CHICKEN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRAIA; TETRAPQDA; AVES; NEOGNAIHAE;
                                                                                                                                                                                                                                                                                                                                                                                          THE INITIAL STEP IN THE SYNTHESIS OF DOLICHOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 GLEVGOCIVLAILALLNDLLYFSMGPLATRDSHRFSAVLIIPFLGVSLALWKWNRWPATV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GLSPGOVIIVRGL-VLQEPKHFTVS-LRDQAAHA-PYTLRASFADRTLA-WI-SRWGQKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATEWAY: GLYCOSYLATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                            P-P-QLIGOSACCHARIDES.
-!- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + DOLICHYL.
PHQSPHATE = UMP + N-ACETYL-D-GLUCOSAMINYL-DIPHOSPHODOLICHOL.
-!- ENZYME REGULATION: INHIBITED BY TUNICAMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 86130505.
OHTAWA Y., HIRABAYASHI J., ODA Y., OHNO S., KAWASAKI H., SUZUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; L0000078; ALG7.
TRANSFERASE; GLYCQSYLTRANSFERASE; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 DOLICHOL RECOGNITION (POTENTIAL) 50368 MW; EFC9A131 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: SIGNIFICANT, TO OTHER SPECIES GIPI.
-!- SIMILARITY: SOME TO YEAST ALG1, DPM1, AND SEC19 AND TO EMBL; Y00126; 464885; -.
EMBL; Z00126; 454885; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 106; DB 1; Length 448;
Pred. No. 9.03e-03;
21; Mismatches 32; Indels.
(N-ACETYLGLUCOSAMINE-1-PHOSPHAIE TRANSFERASE) (GLCNAC-1-P
TRANSFERASE) (TUNICAMYCIN RESISTANCE PROTEIN 1).
ALG' OR TURI OR YEB143C OR YEB1628.
SACCHAROMYCES (CEREVISIAE (BAKER'S YEAST).
EURARYDTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                     ALJINOVIC G., POHL F.M., POHL T.M.;
SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- PUNCTION: CATALYSES THE INITIAL STEP IN THE SYNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE, 87203333.
METOG K.O., BISHOP B.;
NUCLEIC ACIDS RES. 15:3627-3627(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%;
ilarity 24.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 FVGDIYCYFAGMVFAVV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 LISAPFLEYPORFFEVL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A27522; A27522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RETICULUM.
                                                                                                                                                                                                                                                                                                           STRAIN-S288C;
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P07583;
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SEQUENCE.

SOTITE SOLUTION OF THE STREET SOLUTION OF THE STREET SOLUTION OF THE SOLUTION

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DEAN C.R., POOLE K.;

DEAN C.R., POOLE K.;

J. BACTERIOL. 175:317-324(1993).

-!- FUNCTION: SPECIFIC RECEPTOR FOR THE SIDEROPHORE FERRIC

ENTEROBACTIN.

-!- SUBCELLUIAN LOCATION: OUTER MEMBRANE.

-!- INDUCTION: REGULATED BOTN BY IRON AND ENTEROBACTIN.

-!- SINLARRIY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROFEINS.

EMBL: M98031 G151435; -- OTHER TONB-DEPENDENT REC. 2; I.

PROSITE; PS00430; TONB_DEPENDENT_REC. 1; FALSE_NEG.

PROSITE; PS01156; TONB_DEPENDENT_REC. 2; I.

ROSITE; PS01156; TONB_DEPENDENT_
                                                                                     Gaps
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSEUDOMONAS AERUGINOSA.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 DVPSAMAIREQLRAGSEIHVRGHVTHKNNKDFSVELLS-GPNI-V-LHVNF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KERSHAW J.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
ENEL; 248621; G728535; -.
WORMPEP: ROTBI.10; CE01627.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
NYPOTNETICAL PROTEIN; GALAPTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.9%, Score 97; DB 1; Length 184;
Best Local Similarity 37.3%; Pred. No. 1.80e-01;
Matches 19; Conservative 11; Mismatches 17; Indels
  Pred. No. 1.30e-01;
15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NDV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NDV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 21.0 KD PROTEIN ROTBI.10 IN CHROMOSOME X.
R07B1.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 184 AA; 20991 MW; EAF0FA73 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
FERRIC ENTEROBACTIN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                               184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALAPTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  Best Local Similarity 33.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K407;
MEDLINE; 93123148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSEUDOMONADACEAE.
                                                                                                                                                                                                     238 QRW 240
                                                                                                                                                                                                                                                            64 SRW 66
                                                                                                                                                                                                                                                                                                                                                                            YRNA_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 15
PFEA_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00509;
                                                                                                                                                                                                                                                                                                                                                                                                          009610;
                                                                                                                                                                                                                                                                                                                                               RESULT YER STATE OF THE PROPERTY OF THE PROPE
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STAIN-ATCC 14405 / ZOBELL;

RX MEDLINE; 91006150.

RA ZUMET W.G., VIEBROCK-SAMBALE A., BRAUN C.;

RL GUR. J. BIOCHEM. 192:591-599(1990).

CC -! FUNCTION: INVOLVED IN COPPER PROCESSING/TRANSPORT.

CC -! SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).

CC -! SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

CC ABC TRANSPORTERS).

DR EMBL; X53676; G45849;

DR PROSITE: PS00211: ABC TRANSPORTER: I.

RW TRANSPORT: ATP-BINDING; COPPER; MEMBRANE.

TRANSPORT: ATP-BINDING; COPPER; MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                         TISSUE-EMBRYO;
MEDLINE; 87250364.
HIRABAYASHI J., KAMASAKI H., SUZUKI K., KASAI K.-I.;
J. BIOCHEM. 101.775-783(1987).
-!- FUNCTION: TANS PROTEIN BINDS BETA-GALACTOSIDE. ITS PNYSIOLOGICAL FUNCTION IS NOT YET KNOWN. IT MAY BE INVOLVED IN THE REGULATION OF DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SÜBÜNIT: MONOMER (USUALLY).
-!- TISSUE SPECIFICITY: MAINLY IN THE INTESTINE (ADULT), MAINLY IN THE SKIN (EMBRYO).
-!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
EMBL: M11674; G211807; -.
EMBL: D00311; G222800; -.
EMBL: D00308; G222800; JOINED.
EMBL: D00309; G222800; JOINED.
EMBL: D00310; G222800; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEUDOMONAS STUTZERI (PSEUDOMONAS PERFECTOMARINA).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION.
BETA-GALACTOSIDE (POTENTIAL).
2A62CF00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 99; DB I; Length 134;
larity 27.9%; Pred. No. 9.41e-02;
Conservative 15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       II GLKPGQRLTVKGIIAPNAKSFVMNLGKDSTHLGLBFNPRFDAB 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P11116; 1SLA.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
GALAPTIN; LECTIN; ACETYLATION; MULTIGENE FAMILY.
KASAI K.-I.;
BIOCHEM. BIOPHYS. RES. COMMUN. 134:51-56(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-CCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
COPPER TRANSPORT ATP-BINDING PROTEIN NOSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 75 BI
134 AA; 14932 MW;
                                                                                                                                             OHYAMA Y., KASAI K.-I.;
J. BIOCHEM. 104:173-177(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JX0042; LNCH14.
PIR; A24062; A24062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                     SEQUENCE FROM N.A. MEDLINE, 89033999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEUDOMONADACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOSF_PSEST
P19844;
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SEQUENCE Query Match

Best Loc Matches

셤 ò RESULT

BINDING

4

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1; Gaps
                                                                   Ouery Match 9.7%; Score 95; DB 1; Length 746; Best Local Similarity 37.8%; Pred. No. 3.42e-01; Matches 14; Conservative 10; Mismatches 12; Indels
39 44 TONB BOX.
729 746 TONB C-TERMINAL BOX.
746 AA; 80967 MW; 3BC231B9 CRC32;
SIMILAR
SIMILAR
SEQUENCE
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Search completed: Tue Dec 15 15:55:27 1998 Job time : 16 secs.

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n.a. - n.a. database search, using Smith-Waterman algorithm

Tue Dec 15 18:30:42 1998; MasPar time 1134.44 Seconds 1365.449 Million cell updates/sec Tabular output not generated.

Run on:

>US-09-109-864-1 (1-865) from US09109864.seq 865 Title: Description: Perfect Score: N.A. Sequence: Comp:

......адаввааааааааааааа 865 1 tttgtggagggcagcagaga.

TABLE default Gap 6 Scoring table:

Query 0 Dbase 0; .. Nmatch STD

2275026 seqs, 895388244 bases x 2 Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

embl-est55 Database:

Database:

5:92.est1 6:92.est10 7:92.est11 8:92.est12 9:92.est13 10:92.est14 11:92.est15 12:92.est16 13:92.est17 114:92.est18 11:92.est19 16:92.est2 17:92.est27 118:92.est21 19:92.est3 20:92.est4 21:92.est5 22:92.est6 23:92.est7 24:92.est8 25:92.est9 26:92.gss1 27:92.gss2 28:92.gss3 29:92.gss4 1:em_est1 2:em_gssl 3:em_gss2 4:em_gss3 genbank-est107

Mean 12.059; Variance 7.331; scale 1.645 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB ID Description
AA311108
H30148
H27468 yo59h05.sl Homo sapien
AA349100
AA020729
AA001029
AA754459
AA754459
R37188
C84867
AI128239
AA754458
C24325

Bioinformatics The Institute for Genomic Research

Other_ESTs: THC124424 Contact: Kerlavage, AR

JOURNAL MEDITINE COMMENT

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RESULT
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                       Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org

information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgl.html)
Seg primer: M13 Reverse.
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9712 Medical Center Drive, Rockville, MD 20850
Tel: 3018699056
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Homo saplens cDNA clone 182265 5'
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/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
.>496
a 143 c 151 g 103 t
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                                                                                                                          /organism="Homo sapiens"
/note="Vector: pBluescript SK-;
XhoI"
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                                                                     Bento Soares
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soare and M.Fatima Bonaldo.
                                                                                                        Homo sapiens

Eukaryotae; Metazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gardhostomata; Osteichthyes;
Deuterostomia; Chorada; Tertapoda; Ammiota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 411)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

"Tevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estëwatson.wustl.edu
High quality sequence stops: 264
Source: IMAGE Consortium, LINL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1810
Fax: 314 286 1810
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DEFINITION yo59h05.s1 Homo sapiens cDNA clone 182265
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Pred. No. 2.64e-199;
0; Mismatches 13;
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/clone="182265"
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l Similarity 95.7%;
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                                        Deuterostomia; Chordata; Vertebrata; Chathostomata; Osteichthyes; Sarcopterygii; Chordata; Vertebrata; Chathostomata; Chordata; Vertebrata; Chathostomata; Theria; Sarcopterygii; Chonata; Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Archorda; Primates; Catarrhini; Hominidae; Homo.

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hulman, M., Kucaba, T., Ee, M., Cennos, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 309
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                      Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Pred. No. 1.39e-187;
0; Mismatches 26;
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The WashU-Merck EST Project
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L Chases 1 to 227)

S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoglagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Moreno-Palanques, R.F., WcDonald, L.A., NGUYen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Fang, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Yu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haselline, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Vertebrata, Mammalia, Eutheria, Primates; Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                       AA349100 227 bp mRNA EST 21-APR-1997 EST55685 Infant adrenal gland II Homo sapiens cDNA 5' end, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/organism="Area" adrenal gland; Vector: pBluescript SK-;
Site_1: EcoR1; Site_2: XhoI"
/db_xref="ArCC (inhost):150218"
/db_xref="taxon:9606"
359 TCCCGCANCIGCTCCAGGGGCCIGCTGGTTCANGCTGGTGGGCCCCCCAGNCCCTNCCCAT 418
                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 221; DB 25; I
Pred. No. 1.44e-120;
0; Mismatches 4;
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/dev_stage="infant, 16 wks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 09
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Contact: Kerlavage, AR
Bioinformatics
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ilarity 98.2%;
Conservative
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Query Match 13.9%;
Best Local Similarity 96.2%;
Matches 150; Conservative
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The WashU-Merck ES
Unpublished (1995)
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AUTHORS
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WashGreat EST Project
WashGround Fark WashGreat Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is avallable royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSert Length: 2180 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 444.

Coctaining "Homo sapiens"

1. .660
/organism "Homo sapiens"
/organi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO20729 660 bp mRNA EST 30-JAN-1997 2e63all.rl Soares retina N2b4HR Homo saplens cDNA clone 363644 5' similar to contains Littl Li repetitive element; mRNA sequence. AAO20729
                                                                                                            61 ACAIGCTCTTCCCCAGGGTCTCTCGCCTGGGCAGGTCATCATAGTACGGGGACTGGTTT 120
                                                                                                                                               GCAAGAGCCGAAGCATTTTACTGTAAGCCTGAGGGACCAGGCTNCCCATGCTCCTGTAAC 180
                                                                                                                                                                                                                                                            Homo saplens

Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Bukaryotae; Eutherla; Primates; Catarrhini; Hominidae; Homo.

Losses I to 660)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rikin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Wash Wash Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                           /clone="363644"
/clone_lib="Soares retina N2b4HR"
/sex="male_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                           181 ACTCAGGGCCTCCTTCGCAGACAGAACINTGGCCTGGATCTCCCGCT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 t
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147 c
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ze46bl2.rl Soares retina N2b4HR Homo sapiens cDNA clone 362015 5' similar to contains Alu repetitive element; contains Ll.tl Ll repetitive element; mRNA sequence. AA001029 g14.77096
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2264 Std Error: 0.00
                                                                                                                                                                                331 ctgaagctggcgctcaatgggcagggctgggggccaccagcatgaaccagcaggcctg 390
                                                                                                                                                              60 GAGCAGCTGCGNGA-CTCCGGATCAGTGGAAGTGTCCAGCTCTACTGTGTGTCCACTCCTGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 434)
Hillier.L., Clark.N., Dubuque.T., Elliston.K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra.M.,
Parsons,J., Rikkin.L., Rohlfing.T., Soares,M., Tan.F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                               1 CTGAAGCTGGCGCTCAATGGGCAGGGGCTGGGGGC - ACCAGCATGAACCAGCAGGCCCTG 59
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
WashU-Werck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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      Length 660;
                                        Indels
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/clone="362015"
/clone=lb="soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
Score 120; DB 22; L
Pred. No. 2.17e-53;
0; Mismatches 1;
                                                                                                                                                                                                                                      Seq primer: mob.REGA+ET
High quality sequence stop: 345.
Location/Qualiflers
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Poales; Poaceae; Oryza.
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ORIGIN
                                                         131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                              AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
92801165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Woctor: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza
1 (bases 1 to 252)
Nahm, B.H., Kim, W.Y., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, W.Y., Kim, W.Y., Yang, W.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="975N1787"
/clone="975N1787"
/clone=lib="Rice Immature Seed Lambda 2APII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                           377 accagcaggccctggagcagctgcgggagctccggatcagtggaagtgtccagctctact 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 NVSGDWHYWBVBNTKVDVGNHTRC-SRWRBVTRMAHYHDYTNCBBYNNDYHWWHBBMYB 130
                                                                                                                                                                                           1 ACCAGCAGGCCCTGGAGCAGCTGCGNGA-CTCCGGATCAGTGGAAGINTCCAGCTCTACT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CCCBAMMITSYBCHGNBVWVCVASHGNYMSVHN-CIBRGIHCDCRNVNWSIMIWGIVNWB 71
                                                                                                                                                         Gaps
                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                      GTGTCCACTCCTGA-GGATGGTTCCAGGGAAATACCGCCAGAAACAAGA 108
                                                                                                                                                                                                                                                                                      Length 434;
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                                                                                                                                                     2; Indels
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                                                         4 others
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/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Cytogenetics
National Inst. of Agri. Sci. and Tech. RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                               Score 80; DB 22; I
Pred. No. 4.14e-28;
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                                                                                                                                                     0; Mismatches
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                                                                                                             Query Match 9.2%;
Best Local Similarity 94.5%;
Matches 104; Conservative
                                 <1. >434
a 104 c
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AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
4A754459 92801165
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/organism="Oryza sativa"
/oultivar="Milyang33"
/note="Vector: pBluescript SK(+); Site_1: EcoR1; Site_2:
**Not: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoR1 and 3' end with Xho I site."
/db_xref="taxon" 4330"
/clone="975N1787"
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kynngdido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 bail: myean@sun20.asii.re.kr
Submitted by Baek Hie Nahm, Dept of Blological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 252)
Nahm.B.H., Kim.J.K., Cheong.J.J., Kim.S.I., Hahn,T.R., Moon,E.P.,
Kim.W.T., Kim.W.Y., Yang.M.S., Park.R.D., Sohn,U.I., Kang.K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                               652
                                                                                           BIGCMICTMWCWBHINIKCIASGWHISINNDVKSSINIWGVIBSYDKSMHGYWCSBBVKY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 MSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRB 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVKSSTNTWGV-TBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCVRKYCVMWMTKKVV 219
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      712 ctgtgagtgcagtccaggccctgaaggcagatggagccatatcccaggctcctggtggag
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                                                                                                                                                                                                                  191 HIKVSTTRAIRSYTCVRKYCVMWMIKKVVKKYHVVBBGCHBIDS 234
78;
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Local Similarity 10.0%; Pred. No. 2.79e-13;
hes 21; Conservative 109; Mismatches 78.
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SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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A1128239 492 bp mRNA EST 11-SEP-1998 qc33f09.x1 Soares_pregnant_uterus_NDHPU Homo sapiens cDNA clone IMAGE:1711433 3' similar to qb:M69520 CELL DIVISION PROTEIN KINASE 2 (HUMAN); contains element MSR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/forganism="Corgan: uterus: Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco NI: 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
AACTGGAAGAATTCGCGCCCCTTTTTTTTTTTTTTT 3')
AACTGGAAGAATTCGCGCCCCTTTTTTTTTTTTTT 3')
(Pharmacia), digested with Not I and cloned into the Not and Eco NI sites of the modified pT7T3 vector. Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (07-JAN-1998) to the DDBJ/EMBL/GenBank databases.
Grushihara, University of Tsukuba, Institute of Biological
Sciences; 1-1.1 fan-noudai, Tsukuba-shi 305-0006, Japan
(E-mail:qxurushi@bank.dna.affrc.go.jp, Tel:+81-0298-53-4664,
Fax:+81-0298-53-6614)
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
1. 341
                                    Mizuno,H., Morio,T. and Tanaka,Y.
Developmental CDNA in Dictyostelium discoideum (229)
Unpublished (1998)
2 (Dases I to 341)
Urushihara,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                          /organism="Dictyostelium discoideum"
  Eukaryotae; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 12; Pred. No. 1.77e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                /strain-"AX4"
/db_xref-"taxon:44689"
/clone_lib-"SS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
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29 c 35
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Best Local Similarity 77.2%;
Matches 71; Conservative
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Unpublished (1997)
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                     (sites)
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                                                                                                                                                                                                                           Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 448)
Hillier,L., Clark, N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
High quality sequence stops: 306
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
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Washngton University School of Medicine
Washngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST; EST(expressed sequence tag).
Dictyostellum discoideum (strain:AX4) slug cDNA to mRNA.
clone_llb:SS.
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Dictyostelium discoldeum slug CDNA, clone SSG869,
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                                                                                                                           448 bp mRNA EST
Homo sapiens cDNA clone 137566 5'
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    .448
    /organism="Homo sapiens"

220 KKYHVVBBGCHBTDSKCKTMWMTNKHVMTS 249
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The WashU-Merck EST Project
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86 c 9
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Best Local Similarity 91.9%;
Matches 56; Conservative
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403 gagctccggatcagtggaagtgtccagctctagcgatggttcca 462
     9 VWRGCCCCBAWMNXHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBW
                                                                                                                                                                                                                                                                                                                                                                                                                                      to mRNA, clone_lib:FC.
Dictyostelium discoideum
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Best Local Similarity 90.2%;
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa alona clone 97SN1784, mRNA sequence.
AA754458
92801164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa

Eukaryotae; Viridiplantae; Charophyta/Embryophyta grbup;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PBJuescript SK(+); Site_1: EcoRI, Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon 1530"
/clone="97SN1784"
/clone="97SN1784"
/clone=libr"Rice Immature Seed Lambda ZAPII cDNA Library"
/dssue_type="Immature Seed"
/dev_statype="Immature Seed"
/dav_statgqe="5 days after pollination"
/lab_host="E. coli SOLR"
lab_host="E. coli SOLR"
lab_host="E. 21 g 34 t 169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer
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                                                                                                                                                                                                                                                                                         17 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAACTAGGCCCATTTTTAAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-1998
                                                                                                                                                                                                                                       Gaps
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went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

cdb_xref="taxon:9606"

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/clone="ixaon:1711433"

/clone_lib="Soares_pregnant_uterus_NbHPU"

/dev_stage="adult"

/lab_host="bH10B"
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Pred. No. 6.32e-10;
114; Mismatches 87; Indels
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National Inst. of Agri. Sci. and Tech, 18 Swon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                               131
                                                                                                                                                                                                                                                                                                                                                              77 GGGCCACAAACTAAATTACAAAAAAGGTTAAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Oryza sativa"/cultivar-"Milyang23"
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Pred. No. ]
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Best Local Similarity 11.6%;
Matches 27; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 bp
                                                                                                                                                                                                Match 5.8%;
Local Similarity 77.2%;
Nes 71; Conservative
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C24325 558 bp mRNA EST 09-JUN-1997
Dictyostelium discoideum gamete cDNA, clone FC-AQ23, mRNA sequence.
C24325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-MAY-1997) to the DDBJ/EMBL/GenBank databases. Hideko Turahihara, University of Tsukuba, Institute of Biological Sciences; Ten-noudai 1-1-1, Tsukuba-shi, Ibaraki-ken 305, Japan (E-mail:d402hussakura.cc.tsukuba.ac.jp, Tel:0298-53-4664, Fax:0298-53-6614)
                                                                                                                                                                                                                                                                                                                                                                                         g2190079
EST; EST(expressed sequence tag).
Dictyostelium discoideum (strain:KAX3) Sexually mature Gamete cDNA
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MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 YYARSKYGYGTBYYSWNVDINIGGIGVGKITVNVHSGWNNRCSNSVVYVWB-TAYCDYBH 127
                                                 521
                                                                                                                       128 YBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRV-TGYDKTDSDCGGGGWRKVTYGSSB
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EST: EST(expressed sequence tag).
Dictyostelium discoideum (strain:AX4) slug cDNA to mRNA,
clone_lib:SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                 187 YBRCG-VNVAVRTISMWTDKSTKMBSMDMSRRSRVHYGRHMBNKKRGMSRNW 237
                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 558;
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Pred. No. 6.32e-10;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C90955 151 bp mRNA EST
Dictyostellum discoideum slug cDNA, clone SSJ350,
C90955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Dictyostellum discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (sites)
Sazukk,K., Shimizu,H. and Urushiihara,R.
Sexual cDNA in D. discoldeum
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Sexually mature"
67 c 94 g 172 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="kAx3"
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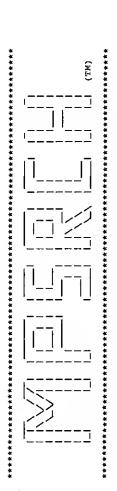
```
Direct Submission
Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases. Hideko
Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases. Hideko
Sciences; 1-1-1 Ten-noudai, Tsukuba-shi 305-8572, Japan
(E-mail:qxurushidbank.dna.affrc.go.jp, Tel:+81-0298-53-4664,
Fax:+81-02996-53-6614)
PROJECT - Dictyostellum discoideum cDNA project in Japan'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C90027 241 bp mRNA EST 15-APR-1998 .
Dictyostellum discoideum slug cDNA, clone SSG112, mRNA sequence.
C90027
                                                                                                                                   Distract Submission
Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases.
Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases.
Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases.
Science; Nakamachi 337, Nara 631, 3ppan
(E-mail:yoshida@ews06.nara.kindai.ac.jp,
Tel:+81-742-43-5131(ex.3005), Fax:+81-742-43-1155)
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
Location/Qualifiers
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Dictyostellum discoideum (strain:AX4) slug cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                       2 others
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Pred. No. 2.23e-09;
0; Mismatches 20; Indels
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                                                           Developmental cDNA in Dictyostellum discoideum
Published Only in DataBase (1998) in press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental cDNA in Dictyostellum discoldeum
Published Only in DataBase (1998) In press
2 (bases 1 to 241)
                                                                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum"
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    241
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Dictyostellum discoideum
Eukaryota: Dictyostellida: Dictyostellum.
1 (bases 1 to 241)
Urushihara, H.
Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostelium
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Pred. No. 2.23e-09;
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/db_xref="taxon:44689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         838 aaaaaaaaaaaaaaaaa 865
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l c 5 c
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Best Local Similarity 77.3%;
Matches 68; Conservative
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Best Local Similarity 90.0%;
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                                   1 (sites)
Yoshida, M.
                                                                                                                           Coshida, M.
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SOURCE
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Search completed: Tue Dec 15 18:57:34 1998 Job time : 1612 secs.



Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tue Dec 15 18:00:04 1998; MasPar time 1259.73 Seconds 1513.252 Million cell updates/sec Run on:

rabular output not generated.

>US-09-109-864-1 (1-865) from US09109864.seq 865 Title: Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD:

567134 seqs, 1101898692 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

emb155
l:em_ba_2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_ov 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vi
genbank107
15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
21:gb_pat 22:gb_ph 23:gb_pl 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts
32:gb_un 33:gb_vi Database:

Mean 11.899; Variance 15.521; scale 0.757 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		of.					
Result No.	t . Score		Query Match Length DB	DB	CI ,	Description	Pred. No.
Ü	1 477	55.1	35414	26	073641	Human Chromosome 11 Co	2.20e-137
	2 54	6.2	2982	23	DDISGSPA	Dictyostellu discoideu	3.81e-04
	3 48	5.5	1927	52	HSEPMG50	H.sapiens mRNA for 50	1.50e-02
-	4 48	5.5	2787	18	PFSTARP	P.faiciparum gene for	1.50e-02
	5 . 48	5.5	244649	17	AC005308	*** SEQUENCING IN PROG	1.50e-02
_	6 47	5.4	144	7	I89947	Sequence 26 from paten	2.74e-02
•	7 47	5.4	766	21	108319	Sequence 1 from Patent	•
U	8 47	5.4	2606	23	DDICAR	Dictyostellum discoide	
O	9 47	5.4	10772	18	AF012089	Drosophila melanogaste	2.74e-02
Ä	9 0	5.3	460	18	AF026266	Lucilia cuprina cuticl	4.97e-02
H	1 46	5.3	1744	23	ATPYK10	A.thaliana mRNA for th	4.97e-02
H	2 46	S.3	1999	58	MMU80780	Mus musculus putative	4.97e-02
H	3 46	5.3	3795	13	BTU73585	Bos taurus Fanconi ane	4.97e-02

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complement(18065. .18328)
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Direct Submission
Submitted (17-APR-1990) Herbert L. Ennis, Roche Institute of
Molecular Biology, 340 Kingsland Street, Nutley, NJ 07110-1150, USA
Shaw, D.R.
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Submitted (18-JUL-1995) David R. Shaw, Roche Institute of Molecular
Submitted (18-JUL-1995) David R. Shaw, Roche Institute of Molecular
Biology, 340 Kingsland Street, Nutley, NJ 07110-1150, USA
On Aug 1, 1995 this sequence version replaced gi:167880.
Location/Qualifiers
1. 2982
/.crgan.sm="Dictyostelium discoideum"
/strain="AX-3"
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( Chases 1028 to 2982)

Glorda,R., Ohmachi,T., Shaw,D.R. and Ennis,H.L.

Shared internal threonine-glutamic acid-threonine-proline repeat
defines a family of Dictyostellum discoideum spore germination
specific proteins
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                                                                                                                                                                                                                                                                                                                                                   aaggtgcagagttcgaggaacctttgcactcttgtgccttccctcaggcccaaagctcct 592
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                                                                                                                                                                                            TGTGAGTGCAGTCCAGGCCCTGAAGGCAGATGCAGCCATATCCCAGGCTCCTGGTGGAGG
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                                                                                                                                                                                                                                                                                spore germination-specific protein. Dictyostellu discoideum (strain AX-3) cDNA to mRNA and
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Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
Dictyostelium.
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Pred. No. 2.20e-137;
0; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 523; Conservative
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                                                                                                                                                                                                                            //note="spore germination-specific protein; formerly called
270-11"
                                                                                                                                                                                                                                                                                                                                  /product="cellulose binding protein"
/db_xref="PID:g167881"
/translation="MKNIYSLFLLFALISATFANNAFIVHWNSDSISKKLFGQ1GDFI
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H.sapiens mRNA for 50 kDa erythrocyte plasma membrane glycoprotein.
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Submitted (23-MAR-1992) K. Ridgwell, University of Bristol, Dept o
Biochemistry, School of Medical Sciences, University Walk, Bristol
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.81e-04;
0; Mismatches 19; Indels
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                                                                                                                                                                                      join(1196. .1253,1341. .2881)
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1254. .1340
/gene="CelB"
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/gene="CelB"
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/db_xref-"taxon:9606"
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Biochem. J. 287 (Pt 1), 223-228
'db_xref-"taxon:44689"
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/gene="CelB"
                                                                              /gene="CelB"
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Best Local Similarity 79.3%;
Matches 73; Conservative
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BIFKASDIGASMTILAFGAYFGLAVAGILYBSGLRKGHENESSAYSDLFAMIGTLFL
WHEWPSFMSAIAEPGDKQCARIVDTYFSLAACVLTAFAFSSLVEHRGKLNWHIONAT
LAGGYAVGTCALWATHEPGSYLIGSIAGMYSVLGYRFLPLFTKLKIHDTGCYHNLH
GLPGVVGGLAGIVAVAMGASNTSMAMQAAALGSSIGTAVVGGLATGLILKLPLMGQPS
                                                                                                                                                                    /product="50 kDa erythrocyte plasma membrane glycoprotein"
/db_xref="PiD:931195"
                                                                                                                                                                                                                                                    /translation-"mreteplialylelamivi.egleveyetoctveolnitkp.dm
GIFFELXPLFODVHVMIFVGEGFLATPLKKYGFSSVGINLLVAALGLQWGTIVOGILO
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Fidock, D.A.
Fidock, D.A.
Direct Submission
Submitted (16-SEP-1993) David A. Fidock, Laboratory of bio-medical
parasitology, Pasteur, Institute, 25, rue du Dr. Roux, Paris,
PARIS, 75724 CEDEX 15, France
Location/Qualifiers
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1 (bases 1 to 2787)

2 (bases 1 to 2787)

2 (bases 1 to 2887)

2 (bases 1 to 2887)

3 (bases 1 to 2887)

3 (bases 1 to 2887)

4 (bases 1 to 2887)

5 (bases 1 to 2887)

5 (bases 1 to 2887)

6 (control and characterization of a novel Plasmodium falciparum sporozolte surface antigen, STARP

6 (control and characterization)

6 (control and characterization)
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/db_rref="taxon:5833"
/clone="DG21"
/dev_stage="Sporozoite, liver stage, erythrocytic ring stage"
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Plasmodium falciparum
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Pred. No. 1.50e-02;
0; Mismatches 8; Indels
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/standard_name="glycosylation site"
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                    /tissue_type="bone marrow, liver"
/chromosome="6"
/map="6p21-qter"
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/organism="Plasmodium falciparum"
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/dev_stage="foetal"
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*** SEQUENCING IN PROGRESS *** Plasmodium falciparum 3D7 chromosome
12 PFYAC492 genomic sequence, HTGS phase 1, 36 unordered pieces.
AC005308
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DNDNNTKISTDNNTKTISDNNNNTNTSTONNNNTNÖYVFANNTRETSDBELNK
DSCDYSEEKENIKSTLDKLDLETVRK HSDISTCIEKKNNPRNQITHLNNLKNN
YNIIKFIVVIYIAFNWSEVIYKYVGKLILAFALYMLIN
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Kpidnintdikstdnyntgiketdiknidikatdninitttidntnyistdnsktn
                                                                                                                                /db_xref="PID:9499325"
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LAANNSTTTSTTKVTDNNKTNIKLTGNNSTTINTNSTENTSATKKVTENVITNQILTG
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Submitted (21-JUL-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases I to 2446.4)
Hyman, R.W., Qin, F. Pung, E.L., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
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Pred. No. 1.50e-02;
0; Mismatches 20; Indels
/cell_line="T9/96 blood stage culture"
/clone_lib="Lambda gt11"
                                                               join(1. .806,982. .2787)
/product="STARP antigen"
join(735. .806,982. .2724)
                                                                                                                   'product-"STARP antigen"
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malaria parasite P. falciparum.
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                        /chromosome="8"
1. 806
/number=1
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982. .2787
/number=2
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Best Local Similarity 77.3%;
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US-09-109-864-1.rge

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AF012089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cas, and phenylalanyl tRNA synthetase gene, partial cds. 4F012089
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="extreme transcription initiation at -1593 relative
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1274. .2071
/note-"extreme transcription initiation at -535 relative
to the AUG translation start codon; promoter element
between positions -694 and +103 relative to transcription
initiation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                to the AUG (2604-2606) translation start codon; promoter element between positions -1010 and +283 relative to transcription initiation"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Trachoata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 4546 to 4553)
                                                         DDICAR 2606 bp DNA PLN 14-JUN-1994
Dictyostelium discoideum cAMP receptor (CAR1) gene, 5' flank.
L09637
                                                                                                                                                                                                            1 (bases 1 to 2606)
Louis,J.W., Saxe,C.L. III. and Kimmel,A.R.
Two transmembrane signaling mechanisms control expression
AMP receptor gene CAR1 during Dictyostellum development
Proc. Natl. Acad. Sci. U.S.A. 90 (13), 5969-5973 (1993)
93317605
 cAMP receptor.
Dictyostellum discoideum (strain Ax-3) DNA.
Dictyostellum discoideum
Eukaryotae; mitochondrial eukaryotes; Dictyostellida;
Dictyostellum.
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Pred. No. 2.74e-02;
0; Mismatches 7; Indels
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/strain="Ax-3"
/db_xref="taxon:44689"
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/note="early mRNA"
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/note="late mRNA"
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Best Local Similarity 88.5%;
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Jacobs, K., McCoy, J.M., LaVallie, E.R., Racie, L.A., Merberg, D., Treacy, M. and Spaulding, V.
Secreted proteins and polynucleotides encoding them
Patent: US 5723315-A 26 03 MAR-1998;
Location/Qualifiers
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Mahoney,W.C.
PRODUCTION OF MATURE PROTEINS IN TRANSFORMED YEAST
Patent: WO 8401173-A 1 29-MAR-1984;
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Pred. No. 2.74e-02;
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Pred. No. 2.74e-02;
0; Mismatches 5;
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/chromosome="12"
25158 c 27624 g 92761 t 12
                                                                                                  Score 48; DB 17; 1 Pred. No. 1.50e-02;
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Sequence 26 from patent US 5723315.
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Sequence 1 from Patent WO 8401173.
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Best Local Similarity 77.3%;
Matches 68; Conservative
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Best Local Similarity 87.7%;
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/db_xref="Tib:g3305221"
/db_xref="Tib:g3305221"
/db_xref="Tib:g3305221"
/fb_xref="Tib:g3305221"
/fb_xref="Tib:g3305221"
/fb_xref="Tib:g3305221"
/fb_xref="Tib:gaylup"
/gradDesproteing-paylib|/fb-xref="Tib:gaylup"
/gradDe
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/db_xref="PlD:92305222"
/db_xref="PlD:92305222"
/translat.con="Milly trny Garhwikstrclassaapakspssppolevsgstya
TDG#TNWTPKILSYYGANKHLOTBED.SIIRORIVNYFYGAYRNGGNPLFSYYDQMN
PVVTVQQNFDNILIPADHVSRQKSOCYYINQQHILRAHTTAHQVELISGGLDNFLVVG
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SSWYKRDSATRRANKLMEHENKHVLVGLTRDLFGPRIKTRWDTYFPFTQFSKELLEI
YFRDWHLEVLGCGIMRHEILDRSGVHQSIGTARGVGLERLANVLFDIPDIRLFWSDDS
GFLSQPESERLLHULFKKYPIEHTPQCTNDLSFWLPQDIEVDAGFSPNDFTDLVSGVAG
DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
Gray,Y.H., Tanaka,M.M. and Sved,J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                University
                                                                                                                                                                                                                                                                                  Unpublished

(Gray, Y.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.)

(Bray, H.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.)

Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University (Bydney, Blology Al2, Sydney University, NSW 2006, Australia Location/Qualifiers

1. 10772

/db.xref="taxon:7227"
/db.xref="taxon:7227"
/gene="CP1"
                                                                                                                                                        Chases 1 to 10772)
Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
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/gene="CP1"
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join(8110. .9300,9370. .>9532)
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872. .7707
                                                                                            Genetics 144 (4), 1601-1610 (1996)
97132596
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/gene="CP1"
/note="insertion site of
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6476. .6690
/gene="CP1"
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/gene-"CP1"
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/gene="CP1"
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/gene="CP1"
2310. .2426
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/gene="CP1"
4546. .4553
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/gene="CP1"
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/product-"cuticle 12 homolog"
db_xref="PID:92565394"
/translation-"REINVEALENVALAAPRPEDATVLRSESEVGPESFOYSYATS.
DGVEAEADGQLKNVGTDEEAIVVKGSFSFVADDGQTYTVNYVADENGFOPQGAHLDVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Lucilia.

1 (bases 1 to 460)
Casu, R.E. and Jarmey, J.M.
Direct Submission
Sibmitted (22-SEP-1997) Tropical Agriculture, Commonwealth Scientific and Industrial Research Organisation, 120 Meiers Road, Indooroopilly, QLD 4068, Australia
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                                                                                                                                                AF026266 460 bp mRNA INV 28-OCT-1997 Lucilla cuprina cuticle 12 homolog (cut12) mRNA, complete cds. q2565393
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Pred. No. 4.97e-02;
0; Mismatches 25; Indels
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                                                              Score 47; DB 18; Le
Pred. No. 2.74e-02;
69; Mismatches 50;
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/db_xref="taxon:7375"
                3046
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/gene="cut12"
/codon_start=1
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32. .349
                                                              Query Match 5.4%;
Best Local Similarity 19.0%;
Matches 28; Conservative
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Best Local Similarity 74.0%;
Matches 71; Conservative
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ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

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AUTHORS REFERENCE

TITLE

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/product="Fanconi anemia group C protein"
/db_xref="PID:92326996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467 t
                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
1. :1999
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                                                                                                                                                                                                                                                                                                         /note="similar
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                                                                                                                                                                                                                                               'gene="HD1"
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Best Local Similarity 91.1%;
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="thioglucoside glucohydrolase"
/db_xref="PID:g984052"
/db_xref="PID:g984052"
/translation="MYLOKEPLIGLILLITYASPANADGPVCPPSNKLSRASPPEGF
LFGTARAAXOVEGA.HWTCRGPALWITYCRRYPERCNNDNGDVAVDFFHRYKEDIQLM
KNLWTDAFRMSIAWPRIFPHGRKEKGVSQAGVQFYHDLIDELIKNGITPFVTVFHWDT
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BRCSSYVMAKQOGBSGYEALLVHHALLISHBARAVEAYKOEKCKGGYGGKAIGHABSPAW
PEAHDLADSQDGASIDRALDFILGWHLDTTFFGDYDQIMKDIYGHRLPKFTFERCKAK.
KASTDFVGLNYYTSVFSNHLEKPDPSKPWMQDSLITWESKNAQNYALGSKPLTAALN
YSRGFRELLKYIKDKYANPELMIMENGYGEELGASDSYAVGYADHNRKYYLQRHLLS
MQBAVCIDKYNYYGYFWMSLLDNFEWQDGYKNRFGLYYVDFKNNLTRYEKESGKYYKD
FLSQCYRPSALKKDEL
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Mus musculus putative histone deacetylase (HD1) mRNA, partial cds.
U80780
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Bukaryotae; Metazoa; Chordata: Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases ito 1999)
Johnson, C.A.
Putative histone deacetylase HDI from M. musculus
                                                                          Charophyta/Embryophyta group; Embryophyta: Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.

1 (bases I to 1744)
Schmidt,K.P., Burrows,P.R., Davies,K.G., Kammerloher,W., Schaeffner,A.R., Buck,F., Cai,D. and Grundler,F.M.W. A root specific myrosinase in Arabidopsis responding to cyst nematode infection
                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (04-JUL-1995) K.P. Schmidt, Institut fuer
Submitted (04-JUL-1995) K.P. Schmidt, Institut fuer
Phytopathologie, Hermann-Rodewald-Str. 9, D- 24118 Kiel, FRG
Related sequences: AT4257 and 234217.
Location/Qualifiers
1. .1744
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                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/strain="Landsberg erecta"
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/dev_strage="26 days old"
/tlssue_type="root tissue"
/clone_lib="pcDM8 COS cell expression library"
/clone="full length in pssc Ml3+"
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pyklo gene; thioglucosidase; thioglucoside glucohydr
thale cress.
Arabidopsis thaliana
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
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Pred. No. 4.97e-02;
0; Mismatches 5; Indels
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/EC_number="3.2.3.1"
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1654. 1659
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Schmidt, K.
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Best Local Similarity 91.1%;
Matches 51; Conservative
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BASE COUNT 561
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gene

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AUTHORS TITLE

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KEYWORDS

RESULT

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/product="putative histone deacetylase"
//do_xref="putative histone deacetylase"
//do_xref="putative histone"
//do_xref="putation="MAGTAGTRRXVYYYDGDVGNYYGGGHPMXPHRIRHTHNLLIN
//tanslation="MAGTAGTRRXVYYYDGDVGNYYGGGHPMXPHYRYGENGEDCPV
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LELLKYNGYTYIDIOHHARDOVERAPYTDVRWATVSFHYKOFFFFGFGDLROIGAGK
GXYAPANYPHARGIDDESYEAIFRPYMSKVWEMFGPSAVVLQCGSSGLSGDRIGGTRI
TIKGHARCVEFVKSFNLPMLMLGGGGYTIRNVARCWTYFTAVALDTEIPNELPYNDYF
FSTGPPGFKLHISPSNMYNDWIREJERIKTKQRLEBLINKLPHARGVQMQAIPEDAIPEE
SGDEDEEDDPRISICSSDKRIACEEFFSDSDEGGGGRKNSSNFKKARRYTEDERE
KDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           to human histone deacetylase HDl and yeast
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Bus taurus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora:
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Wong,J.C.Y., Buchwald,M. and Alon,N.
Direct Submission
Submitted (27-1996) Genetics, Hospital for Sick Children, 555
University Ave., Toronto, Ontario M5G 1XB, Canada
Location/Qualifiers
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/db_xref="taxon:9913"
/tissue_type="liver"
/27. .2430
/note="similar to human FAC protein, GenBank Accession Numbers x66893 and x66894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-1997
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Johnson, C.A., White, D., O'Neill, L.P. and Turner, B.M.
Johnson, C.A., White, D., O'Neill, L.P. and Turner, B.M.
Submitselon
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Submitsham, Birmingham B15 2TT, U.K.
On Sep 2, 1997 this sequence version replaced g1:1737470.
Location/Qualifiers
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1 (bases 1 to 3795)

1 (bondy, J.C.Y., Alon, N. and Buchwald, M.

1 (bond, J.C.Y., Alon, N. and Buchwald, M.

1 (Bondy, J.C.Y.)

1 (Bondy, J.C.Y.)
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Bos taurus Fanconi anemia group C mRNA, complete cds
U73585
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Pred. No. 4.97e-02;
0; Mismatches 5;
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KDSLRPEAAACHPATERVVDETERSALLETDGAPEVLAGLQVFTRCFVBALEKENKOL
KFALKTYFPYASPALVMYLLQHPKDLPOGLWHOSLKHISEMLKETVDDHGSYGGPFES
WEFLYHFGRGADITABCOLLAMSBAEASPPEALLMLAFSCSPOAGHOORSKTWVEVKTY
LCCTTKLFRSPARDLQAAAGENLCGDPRPAPACOQLYRLLLHFLLMAPGGHTIAR
EVITIMAQTDAIMNETIGFLDYTLYRWDHLCVBAHRSRKLARELLTETERBQALPGQVN
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LRRMYETLKEMDSNAIIERFPTICQLLAKSCWSPFILAYDESPKILIWCLCCLIKKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF012089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CPI) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. 92305220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray, Y.H., Tanaka, M.M. and Sved, J.A. P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University
of Sydney, Blology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryotae; Metazoa; Arthropoda;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
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0; Mismatches 8; Indels
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/join(872. .1000,2310. .2426,6476. .(/gene="CP1")
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Best Local Similarity 87.1%;
Matches 54; Conservative
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BERFELKTENENKHKTAKHNORFABCKVSFKLAVNKYADLLHHEFROLMNGFNYTLHK
QLRAADESFKGVTFTSPAHVTLPKSYDWRREGAVTAVKDOGGGGGGARAFSSTGALEGO
HEKSGVLYSCLSGONLVDCSTKYGNNGCNGGLMONAFRYTKDNGGIDTEKSYPVALD
DSCHFUNGTVGATDREFTDLFODERKKMARARATVGPVSVALDASHESFOFYSBGVYN
EPOCDAQNLDHGVLVVGFGTDESGEDVWLVKNSWGTTWGDKGFIXMLRNKENOCGIAS
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FYDDWLEVLGCGIMKHEILQRSGVHOSIGYARGVGLERLAWTLEDIDILLFWSNDS
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TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
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Hog cholera virus
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
Pestivirus.
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Hog cholera virus strain Riems polyprotein gene, putative NS5
protein region, partial cds.
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join(2328. .2426,6476. .6690,6751. .7462)
/gene="CP1"
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join(8110. .9300,9370. .>9532)
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Pred. No. 4.97e-02;
73; Mismatches 47;
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                                                         /codon_start=1
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4546. .4553
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Matches 26; Conservative
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1. .472
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/otc="vaccine", C"
/db_xref="taxon:11096"
<1. .216
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1 (bases 1 to 472)
Mueller, H.M., Stark, R., Thiel, H.-J. and Pfaff, E.
Comparison of different hog cholera virus strains: Implications for virul pathogenicity
Unpublished
2 (bases 1 to 472)
Mueller, H.M.
Direct Submission
Submitted (11-JAN-1996) Hubert M. Mueller, Federal Research Centre for Virus Diseases of Animals, Paul-Ehrlich Str. 28, P.O. Box 1149, Tuebingen, D-72001, Germany
Location/Qualifiers
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Search completed: Tue Dec 15 18:30:24 1998 Job time : 1820 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tue Dec 15 18:57:53 1998; MasPar time 127.57 Seconds 922.536 Million cell updates/sec

Tabular output not generated.

Title:

>US-09-109-864-1 (1-865) from US09109864.seq 865 Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Query 0 Dbase 0; •• Nmatch STD

188442 seqs, 68026449 bases x Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

n-geneseq32 Database:

1.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part11 12:part12 13:part13 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 39:part29 30:part20 31:part31 32:part32 33:part33 39:part39 40:part40

Mean 9.274; Variance 8.844; scale 1.049 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	OB	Ð.	Description	Pred. No.
-	47	5.4	166	. 6	N40162	Sequence of prepropar	5.38e-07
2	46	5.3	91	σ	051746	Oligonucleotide probe	1.28e-06
c	45	5.2	3437	21	T31478	Spinach debranching e	3.02e-06
4	44	5.1	1066	œ	049943	Human anti-HBs light	7.13e-06
2	44	5.1	8920	Ξ	062924	Carbamov1-phosphate-s	7.13e-06
o	43	5.0	340	16	099393	Rat allograft inflamm	1.67e-05
ر م	43	5.0	350	16	088660	Rat allograft inflamm	1.67e-05
∞	43	5.0	1078	→	025785	Protein synthesis inh	1.67e-05
6	43	5.0	1136	~	N70435	Sequence encoding ins	1.67e-05
ព	43	5.0	1364	40	V15228	Heterodimeric human i	1.67e-05
11	43	5.0	1364	36	T48099	Human interleukin-12	1.67e-05
12	43	5.0	1396	7	024371	Natural killer cell s	1.67e-05
13	43	5.0	1558	~	Q10896	Encodes Xenopus Bone	1.67e-05

	9.09e-05 9.09e-05 9.09e-05 9.09e-05 9.09e-05
Sequence of murine os a' fragment of clone Human HMGI-C aberrant Rape abscission/dehis Survival motor neuron Human survival motor Human survival motor human survival motor Rape acyl. Acp thioest Sequence encoding ant Clone associated with Plasmid pArG29 (ArC Ligand-Induced gene, Human HI075-I secrete Integrin subunit beta Human extroplasmic dom Alzheimer's disease D Oil seed rape cystein Recombinant activatio Asparaginylendopeptid Asparaginylendopeptid	Human hyaluronan synt Human c-IAPI. Clone Imd2 encoding i Sequence of new plasm Yellowtail tunn DNA e Human mucosal lymphoc Sequence encoding all Human ataxia and rad
0044391 000423 000423 000423 118828 11882	199541 161590 Q05304 N81634 179857 Q53403
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
358 6155 6155 6155 6155 6155 6155 6155 61	2116 2589 3504 3850 3851 3931 5108 8239
	4444444
788 3 3 3 3 3 3 6 5 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	00000000000000000000000000000000000000
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ALIGNMENTS

Prof. 2. Para. 1. Par 16-FEB-1992 (first entry)
Sequence of preproparathyroid cDNA.
Proteclytic cleavage; trypsin; protoprotein; precursor; proteclytic; processing; ss.
Bos taurus. 204 ⊞; Query Match
5.4%; Score 47; DB 3; Length 766;
Best Local Similarity 91.2%; Pred. No. 5.38e-07;
Matches 52; Conservative 0; Mismatches 5; Indels 158 G; 142 C; Location/Qualifiers 1111..460 /*tag= a BP. 262 A; T 1 N40162 standard; cDNA; 766 pleprogrammed YEp-13. W08401173-A.

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Gaps

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Location/Qualifiers
33..743
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1226..8401
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Q62924 standard; cDNA; 8920 BP.
                                                                                                                                                                                            ВР
                                                                                                                                                                              T
Q49943 standard; cDNA; 1066
                 Ouery Match 5.2%;
Best Local Similarity 88.1%;
Matches 52; Conservative
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-0CT-1993.
30-MAR-1993; J00396.
30-MAR-1992; JP-074678.
(SUNR ) SUNTORY LITD.
Arima K, Kurihara T, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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Plasmodium falciparum.
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P-PSDB; R42065.
                                                                                                                                                                                                                                                                                                                                                                      signal_peptide
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                             Q49943;
29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9320205-A
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Matches
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Claim 1, Page 64-67, 90pp; English.

Chartial cDNA clone (731478) codes for a spinach debranching enzyme (DE) (R98371) useful for modifying the branching degree of amylopectin synthesised in plants. It was obtd. by PCR amplification of CDNA (Synthesised in plants.) The clone can be incorporated into a vector DE peptides (R98385-86). The clone can be incorporated into a vector and used for prodn. of recombinant DE, or used in the breeding of transpenic plants; transpenic potatoes showed increased DE activity and produced a starch having altered viscosity and gel stability properties. Ribozyme or antisense sequences can be used to reduce food and industrial appins.

Che DE activity of transpenic plants. The modified starches have food and industrial appins.
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Debranching enzyme: R enzyme; spinach; potato; amylopectin; starch;
transgenic plant; ds.
Oligonuclectide probe MKI4-A consists of nuclectides 5-95 of MKI4 (051735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
                                                                                                                                                                                                                                                                                                                                  New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                      Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 gggccccactctcctccccccatcaaccatccacctgaacaccagcaca 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ssvhsyvvhvvshhhsvhhvvhhvhvvvvhhvvhvvhhvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.3%; Score 46; DB 9; Length 91; 0.0%; Pred. No. 1.28e-06; vative 48; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1995; EOSO91.
22-DEC-1994; DE-447387.
(GENB-) INST GENBIOLOGISCHE FORSCHUNG.
FORMETMAND M. KOSSMAND J, Renz A, Virgin I;
RPI; 96-309595/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 3
T31478 standard; cDNA to mRNA; 3437 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
201..3095
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 14; 23pp; English.
                                                                      Q51746 standard; cDNA; 91 BP.
Q51746;
                                                                                                                                                                                                                                        24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                    31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Conservative
                                                                                                                                                                                                                                                                                               Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R98371
                                                                                                                                                                                                             EP-571911-A.
01-DEC-1993.
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                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                      samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T31478;
                 806
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Polynucleotides encoding the L and H chains of human anti-HBs Ab are given in 049943-3049944. The Ab can be easily produced in large quantities for therapeutic use.

Sequence 1066 BP; 338 A; 274 C; 240 G; 214 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsurnoka N;
                                        Ö
      Length 3437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 5.1%; Score 44; DB 8; Length 1066; Local Similarity 86.7%; Pred. No. 7.13e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1994.

02-DEC-1993; AU0617.

03-DEC-1992; AU-006380.

(UNIX ) UNISEARCH LID.

Flores MV, Osullivan WJ, Stewart TS;

WPI: 94-200271/24.

P-PSDB; R55694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              062924;
06-DEC-1994 (first entry)
Carbamoy1-phosphate-synthetase II.
Carbamoy1-phosphate-synthetase II; CPSII; psCPSII gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurihara T, Matsukura S, Nishihara T,
Score 45; DB 21; Le
Pred. No. 3.02e-06;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                        Human anti-HBs light chain.
Antibody, Ab; light; heavy; chain; hepatitis
HB; surface antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
33..98
/*tag= b
99..740
/*tag= c
/note= "claim 1, page 26"
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DNA encoding allograft rejection factors and immunogenic fragments - useful for identifying transplant rejection inhibitors claim 11: Page 92: 138pp; English.

(99372-Q9933 are rat allograft inflammatory factor 2 (AIF-2) cDNA fragments. The AIF-2 gene is a differentially expressed allograft gene which is expressed in allograft tissue during transplant rejection. Identification of the rat AIF-2 product (R80521) or transplant rejection. Identification of the rat AIF-2 product (R80521) or transcript fragments of this gene and/or the gene product are therefore useful in the diagnostic methods used allow rejection (vascular inflammation) to be detected at an early stage and require only a small amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Sequence given in sequence ID listing in the specification gives nucleotide 111 as C)
Sequence 350 BP; 121 A; 37 C; 63 G; 129 T;
                           Rat allograft inflammatory factor 2 (AIF-2) cDNA fragment.
AIF-2; allograft inflammatory factor 2; transplant rejection;
inhibitor; immunogenic; detection; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 16; Length 350
Pred. No. 1.67e-05;
0; Mismatches 16; Indels
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930..935
/*tag- d
/note- "possible polya signal"
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/note= "possible polyA signal"
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20-DEC-1990; 040954.
20-DEC-1990; DB-040954.
(PLAC ) MAX PLANCK GES FORDERUNG WISSE.
Jach G, Logemann J, Mundy J, Schell J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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10-DEC-1992 (first entry)
Protein synthesis inhibiting gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 8
Q25785 standard; DNA; 1078 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 78.7%;
Matches 59; Conservative
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1..42
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886..1078
                                                                                                                                                                                                29-JUN-1995.
21-DEC-1994; U14724.
21-DEC-1993; US-171385.
(HARD) HARVARD COLLEGE.
RUSSELL ME, UTANS U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1032..1078
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                                                                                                                                      Rattus sp.
WO9517506-Al.
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NPI: 95-240668/31.

PMA encoding allograft rejection factors and immunogenic fragments ruseful for identifying transplant rejection inhibitors

Claim 11; Page 97: 138pp; English.

Claim 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 atttattcatttatttattttttttttttagtttataaaatag-taattctactaatttaa 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the treatment of malaria.

Disclosure; Page 6-16; 31pp; English.

The cDNA sequence encoding the carbamcyl-phosphate-transferase II

The CDSII) of plasmodium falciparum was determined. The CDNA encodes
a protein that includes 2 insert sequences not found in other CPSII
proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSb.

Sequence 8920 BP; 3836 A; 774 C; 1232 G; 3078 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biopsy material. (Sequence ID listing in the specification gives
                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 11; Length 8920;
Pred. No. 7.13e-06;
0; Mismatches 21; Indels 1;
isolated from Plasmodium falciparum, used to develop prods. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09333;
08-FEB-1996 (first entry)
Rat allograft inflammatory factor 2 (AIF-2) cDNA fragment.
AIF-2; allograft inflammatory factor 2; transplant rejection;
inhibitor; immunogenic; detection; diagnosis; ds.
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Pred. No. 1.67e-05;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 ааааааааааааааааааааааааааааааааа 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 ааааааааааааааааааааааааааааааааа 865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 6
Q99393 standard; cDNA; 340 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99380 standard; cDNA; 350 BP. Q99380;
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.1%;
Best Local Similarity 76.3%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.0%;
Best Local Similarity 78.7%;
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21-DEC-1994; U14724.
21-DEC-1993; US-171385.
(HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 tagccataatgaaat 78
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Sequence 340 BP;
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WO9517506-A1.
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Length 350;

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25-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tecombinant DNA procedures for use as growth promoters for enhancing lactation, for stimulating cell proliferation etc.

Tecombinant DNA procedures for use as growth promoters for enhancing lactation, for stimulating cell proliferation etc.

B A 2 base oligonucleotide corresponding to the DNA sequence encoding a A 2 base oligonucleotide corresponding to the DNA sequence encoding.

C amino acids 10 to 23 of mature human IGF-I was synthesized (N70437).

The radiolabeled 42 mer was then employed to screen for IGF-I containing DNA sequences in a human Ilver cDNA library. Insulin.

C like growth factors-la and -18 cDNAs were isolated from a human cDNA genomic gene was isolated and mapped. It encodes at least two preproinsulin-like growth factor-1 proteins. An essentially pure proproinsulin-like growth factor-1 protein comprising the sequence of amino acids shown in Figure six is claimed (P70277).

Sequence 1136 BP; 412 A; 230 C; 268 G; 226 T;
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                                                                                                                                                                                                                                     Pathogen resistant plants prodn. using protein synthesis inhibiting gene—or its fusion products, inserted into the genome, also pharmaceutical use of derived synthesis inhibiting protein bisclosure; Fig 3: 23pp; German.

The sequence is that of a gene encoding a protein which effectively blocks protein synthesis by plant pathogens, e.g. Trichoderma reesis and Fusarium sporotricholdes. It can be fused to active promoters such as wun-1 and the fusion introduced into plant genetic material to impart pathogen resistance to both mono- and di-covyledonous plants. The gene was isolated from mature barley seeds.

Sequence 1078 BP: 276 A; 310 C; 321 G; 171 T;
                                                                                                                                                                                                              Gaps
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Heterodimeric human interleukin 12 subunit 2 encoding cDNA.
Heterodimeric; human; interleukin 12; IL-12; vaccine; antigen;
                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1991 (first entry)
Sequence encoding insulin-like growth factor 1B (IGF-1B).
Growth promoter; lactation enhancer; cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New pre-pro-insulin-like growth factor-1 protein - obtd, by
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                                                                                                                                                                                   Length 1078;
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Pred. No. 1.67e-05;
0; Mismatches 7; Indels
                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                  Score 43; DB 4; LA
Pred. No. 1.57e-05;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                       T 9
N70435 standard; cDNA; 1136 BP.
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06-JAN-1987; 870001.
07-JAN-1986; US-816662.
20-NOV-1986; US-929671.
(UNIW ) UNIV OF WASHINGTON.
                                                                                                                                                                                  Match 5.0%;
Local Similarity 85.2%;
Les 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 5.0%;
Local Similarity 87.7%;
les 50; Conservative
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WPI; 87-200203/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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PT interleukin-12 with antigenic composition.

PS Disclosure; Column 23-26; 23pp; English.

C The present sequence encodes a heterodimeric human interleukin 12

C The present sequence encodes a heterodimeric human interleukin 12

C [IL-12] subunit (putatively the 30 kD subunit) shown in the present specification. The present invention describes a method for enhancing the immune response elicited by an antitgenic composition. The method composition of the imministering IL-12 can be used in therapeutic compositions, e.g. as an adjuvant in vaccines against pathogenic compositions, e.g. as an adjuvant in amount of 0.1 mu g to 0.5 mg per C 5 mu g of antigen, or in cancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic compsn. to improve cell mediated immune response - contains soluble leishmania antigen and interleukin-12 as adjuvant Disclosure; Column 23-26; 22pp; English.

This is the nucleotide sequence encoding the human interleukin (IL)-12 30 kD subunit. IL-12 is a heterodimeric complex composed of the 30 kD subunit and a 40 kD subunit (W07398). The complex is used in a novel immunogenic composition comprising a soluble Leishmania antigen with IL-12, for protection against leishmaniasis. The addition of IL-12 improves cell-mediated immunity by inducing TH1 helper cells (as opposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Human interleukin-12 30 kD subunit gene.

Human interleukin-12 30 kD subunit gene.

Human; interleukin-12 11-12; hererodimeric complex; immunogenic; ds;

Leishmania; antigen; leishmaniasis; cell-mediated immunity; adjuvant;

TH1 helper cell; TH2 helper cell; alum; cytokine; bacterium; cancer;

Vaccine; cell surface; membrane; glycoprotein; antigen presenting cell.

Homo sapiens.
                                                                                                                                                                              /product- "heterodimeric human interleukin 12 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product- interleukin-12 30 kD subunit
                         qs
pathogen; immune response; microorganism; cancer;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 40;
                                                                                                                                                                                                                                                                                                         17-JUN-1994; US-265087.

18-APR-1994; US-229282.

25-MAR-1996; US-621493.

(UYPE-) UNIV PENNSTLYANIA.

(WIST-) WISTAR INST ANATOMY & BIOLOGY.
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17-JUN-1994; US-255087.
(UYPE-) UNIV PENNSYLVANIA.
(WIGT-) WISTAR INST ANATOMY & BIOLOGY.
Scott P. Trinchieri G;
                                                                                       Location/Qualifiers
101..862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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T48099 standard; cDNA; 1364 BP
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Best Local Similarity 90.6%;
Matches 4%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scott P, Trinchieri G; WPI; 98-205996/18.
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RESULT
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to TH2 cells which are induced by alum adjuvant) and does not cause uncontrolled release of other cytokines (in contrast to bacterial adjuvants). IL-12 can also be used as a cancer vaccine by association with the protein B7, a soluble, cell-surface (membrane)-bound glycoprotein which is expressed in antigen presenting cells. Sequence 1364 BP; 446 A; 282 C; 275 G; 361 T;
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1992 (first entry)
Natural killer cell stimulatory factor 30kD subunit.
NKSF: cytokine; gamma interferon; IFN; peripheral blood lymphocytes; IL-2; GM-CSF; granulocyte macrophage colony stimulating factor; PBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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(Laim 12: Page 23: 79pp: English.

NKSF is capable of inducing the production of gamma interferon in human peripheral blood lymphocytes. It has subunits of 40 (R22769) and 30-35 kD (R23729). It is claimed that NKSF is useful in the treatment of bacterial and viral infections e.g. AIDS.

Degenerate probes were designed from tryptic fragments of NKSF and used to screen a cDNA library made from poly A RNA from PGBu induced 8866 cells to identify a cDNA encoding the small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
14..1364
/*tag= //tag= /
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/note= "short clone containg 30kD NKSF subunit"
113..873
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                                                                                                                                                                                                                                                         Query Match 5.0%; Score 43; DB 26; Length 1364; Best Local Similarity 90.6%; Pred. No. 1.67e-05; Matches 48; Conservative 0; Mismatches 5; Indels
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(WIST-) WISTAR INST.
Clark S C, Hewick R, Kobayashi M, Perussia B, Trinchieri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= pro NKFS 30kD subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of NKSF.
See also R22769, Q23586, R23729.
Sequence 1396 BP; 451 A;
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Q24371 standard; DNA; 1396 BP
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Local Similarity 90.6%;
Nes 48; Conservative
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04-SEP-1991; U06332.
18-SEP-1990; US-584941
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WPI; 92-132124/16.
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RESULT 13 ID Q10896 standard; DNA; 1558 BP

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Claim 3: Page 13-17; 34pp; English.
CDAM 11brarles were constructed from the mouse osteoblastic cell
line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
then as much common DNA as possible removed by hybridisation between
the 2 libraries. Residual E1-specific DNA was amplified, inserted
into lambda gil0 and screened by plaque hybridisation. A minibank of
                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis bone morphogenetic protein and DNA encoding itused in therapy of fracture or osteoporosis
Claim 5; Fig 2; 28pp; English.
A Xenopus laevis unfertilised egg cDNA library in lambda gt10 was screened with a Pst-Hindill fragment of X.laevis Xarl4 chromosomal DNA. Three clones were isolated, including clone XDr23 which was found to encode a protein having homology with X.laevis BMP-2B. They were subcloned in pUCl9 and used to transform competent E.coli HB101 cells. Transformant E.coli HB101/pXbr23 coding for the BMP-2B was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   044391;
14-SEP-1994 (first entry)
Sequence of murine OSF-4 cDNA.
OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
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5.0%; Score 43; DB 2; Length 1558;
Best Local Similarity 85.2%; Pred. No. 1.67e-05;
Matches 52; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsujimura A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New bone related, cadherin-like OSF-4 proteins - for trear
and diagnosis of bone metabolic disease, and nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 G;
13-MAY-1991 (first entry)
Encodes Xenopus Bone Morphogenetic Factor BMP-2B.
BMF: osteoporosis; fracture; cartilage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-1993; 113602.
28-AUG-1992; JP-230028.
(FARH) HOECHST JAPAN LTD.
WAMAID E, RAMAIS, OKAZAKI M, Takeshita S,
PP-PSDB; R49730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엺
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q44391 standard; cDNA to mRNA; 3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
284..2671
                                                                                Location/Qualifiers
105..1309
                                                                                                                                             /product= BMP-2B
                                                                                                                                                                                                                                                                   (TAKE ) TAKEDA CHEMICAL IND KK. (SCIT-) SCITECH RESEARCH CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also Q10890-5 and Q10897.
Sequence 1558 BP; 504 A;
                                                                                                                                                                                                                                                                                                         Murakami K, Ueno N, Kato Y;
WPI; 91-075112/11.
P-PSDB; R10996.
                                                                                                                                                                                                                           06-SEP-1989; JP-229250.
20-JUL-1990; JP-190774.
                                                                                                                            /*tag=
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                                                                                                                                                                                                        05-SEP-1990; 117079
                                                             Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                  EP-416578-A
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                                                                                                                                                                                     13-MAR-1991
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This sequence 1s the 3' portion of clone H1075_1, which is a pulsators claim 31; Page 74; 114pp; English.

This sequence 1s the 3' portion of clone H1075_1, which is a polynucleotide of the invention. This sequence was isolated from a human peripheral blood mononucleocyte (PBMC) cDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or confecular weight marker, in genetic fingerprinting, to raise anti-protein or anti-DNA antibodies and in interaction trap assays. The protein can be used to assay biological activity, raise antibodies for use in immunoassays, as marker, to identify inhibitors of its interactions and as a nutritional supplement. It may also have a very wide range of therapeutic and biological activities (no examples are given to support this), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulant or immunosuppressant, haematopolesis tregulator, collicle inhibitor/stimulator, chemotactic/chemokinetic, haemostatic, thrombolytic or anti-inflammatory agent, antimicrobial, haemostatic, thrombolytic or anti-inflammatory agent, antimicrobial, cor positasis treatative.

Sequence 259 BP; 105 A; 19 C; 75 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MXY-1998 (first entry)
3' fragment of clone H1075_1.
3' fragment of clone H1075_1.
Muman; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; clone H1075_1; peripheral blood mononucleocyte; PBMC; ds.
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Pred. No. 3.91e-05;
0; Mismatches 15; Indels 1; Gaps 1;
273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific for El was identified and sequenced. The insert from this clone was used to screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKQT164. This insert was sequenced; it encoded the 796 AA mouse precursor protein (Q44391/R49730). The insert was also used to screen a cDNA bank prepd. from human osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and QSF-4-2 (Q44392/R49731 and Q44393/R49732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid clones from ATCC 98028 encode novel secreted proteins - having many potential uses, e.g. as immunomodulators, cell proliferation or differentiation inhibitors or haematopoiesis regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||| || || || || || || || || || ||| || || ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || ||
                                                                                                                                                                                                                                                                                                                                                                                                    886 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 5.0%; Score 43; DB 10; Length 3581; Local Similarity 90.6%; Pred. No. 1.670-05; Indels (es 48; Conservative 0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-1997.
14-AR-1997, U06134.
14-AR-1996; UG-635311.
(GEM ) GENETICS INST INC.
Jacobs K, Lavallie ER, Mccoy JM, Merberg D, Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                    800 G;
                                                                                                                                                                                                                                                                                                                                                                                                    774 C;
                                                                                                                                                                                                                                                                                                                                                                                                    1121 A;
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V00423 standard; cDNA; 259 BP.
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4.9%;
Best Local Similarity 78.7%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                3581 BP;
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WPI; 97-535776/49.
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                                                                                                                                                                                                                                                                                                                                                            respectively)
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Matches
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Search completed: Tue Dec 15 19:01:29 1998 Job tlme: 216 secs.

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***************************************	 	A John F. Coll (c) 1993-1998 stribution righ	na. database search, us	ne bec 13 19:01:47 1996; not generated.	>US-09-109-864-1 (1-865) from US09109864.seq	ttgtggagggcagcagaga aacacctcccgtcgtctt	TABLE default Gap 6	Dbase 0; Query 0	88822 seqs, 23323279 bases	Minimum Match 0% Listing first 45 summaries	n-issued 1:5_COMB 2:PCT9_COMB 3:bac	Mean 8.740; Variance 6.833	the number of results than or equal to the by analysis of the	SUMMARIES	ery tch Le ngth DB ID	5.1 7218 1 US-08 232- 5.0 340 1 US-08 171- 5.0 1364 1 US-08 171- 5.0 1558 1 US-08-455- 6.0 7218 1 US-08-455- 4.9 3073 2 PCT-US-91-0 4.7 688 3 5498694-3 4.7 198 2 PCT-US-91-0 4.7 2589 2 PCT-US-91-0 4.7 2589 2 PCT-US-91-0 4.7 3933 1 US-08-19- 4.7 3108 1 US-07-642- 4.6 347 1 US-08-10-	.6 2158 1 US-08-261- .6 2158 1 US-07-602-
************	>>	Releas Copyri	MPsrch_nn n.a.	on: .lar output		 	Scoring table:	Nmatch STD:	Searched:	Post-processing:	Database:	Statistics:	Pred. No. is score greater and is deriver	c	Result Qu No. Score Ma	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

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RESULT
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                           625 cactettgtgccttccctcaggcccaaagctcctgtagactcagtctcgt 576
                                                                                            Ouery Match 5.1%; Score 44; DB 1; Length 7218; Best Local Similarity 0.7%; Pred. No. 9.26e-09; Matches 2; Conservative 165; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/08171385
Sequence 27 Application US/08171385
Patent No. 5527884
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: ULIKE Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/171,385
                                                                                                                                                                                                                                                                                                                                                                                     JT 2
US-08-171-385-27 STANDARD; DNA; UNC; 340 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REPERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                     TOPOLOGY: 11near IMMEDIATE SOURCE:
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TELEX: 200154
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Pred. No. 2.65e-08;
0; Mismatches 16; Indels
                                                                                                                                                                Score 43; DB 1; Length 340;
Pred. No. 2.65e-08;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 350
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE 350 BP; 121 A; 37 C; 63 G; 129 T; 0 OTHER.
                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE 340 BP; 114 A; 38 C; 64 G; 124 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
COMPUTER: STRIM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
                                                                                                                                                                                                                                                                                                                                                                                                                                       JT 3
US-08-171-385-14 STANDARD; DNA; UNC; 350 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08171385
Sequence 14, Application US/08171385
Patent No. 5577884
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONIEX/AGENT INFORMATION:
NAME: FRASET, JAILS K.
REGISTRATION NUMBER: 34,819
REFRENCE/COCKET NUMBER: 0542
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 542-8906
TELEX: 200114
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 Franklin S
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                   Query Match
Best Local Similarity 78.7%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.0%;
Best Local Similarity 78.7%;
Matches 59; Conservative
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CLASSIFICATION: 514
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                                              LENGIH: 340
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1527 A 1527
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      865 tttttttttttttttttttttttttttttttttttaaataaataacttatttatttatt 806
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08265087
Sequence 3, Application US/08265087
Patent No. 5571515
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENITON: Compositions and Methods for Use of
TITLE OF INVENITON: 1L-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.0%; Score 43; DB 1; Length 1364; Best Local Similarity 90.6%; Pred. No. 2.65e-08; Matches 48; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                     STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 101..859
SEQUENCE 1364 BP: 446 A; 282 C; 275 G; 361 T; 0 OTHER.
                                                                                                                                                                                                                                   ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/255,087
                                                                           T 4
US-08-265-087-3 STANDARD; DNA; UNC; 1364 BP.
                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MATY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-455-550-7 STANDARD; DNA; UNC; 1558 BP
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                          805 tgaccacaaataaat 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                62 TAGCCATAATGAAAT 76
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DE Sequence 7, Application US/0845550
CC Sequence 7, Application US/0845550
CC Patent No. 567038
CC Patent No. 567038
CC PAPPLICANT: WIRAKAMI, KAZUO
APPLICANT: WIRAKAMI, KAZUO
APPLICANT: WENCY, YUKIO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.0%; Score 43; DB 1; Length 1558; Best Local Similarity 85.2%; Pred. No. 2.65e-08; Matches 52; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
SEQUENCE 1558 BP; 504 A; 328 C; 347 G; 379 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Competible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,550
FILING DATE: 31-MAY-1995
CLASSIFICATION NUMBER: 08/056,564
FILING DATE: 30-APPL-1993
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APPL-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 05-SEP-1990
ATTORNEY-AGENT INFORMATION:
NAME: Eisenstein, Romald I
REGISTRATION NUMBER: 30628
REPERENCE/DOCKET NUMBER: 30628
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Patent No. 5570367 GENERAL INFORMATION: APPLICANT: DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
TELEX: 200291
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTR: 1558 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        02109
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
ID US
AC XX
DT XX
DE SE
CC SE
CC PA
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 ctccttcgcagacagaactctggcctggatctcccgctggggggaggaagaaactgatctc 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                          TELEX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 5.0%; Score 43; DB 1; Length 7218; Best Local Similarity 2.4%; Pred. No. 2.65e-09; Matches 7; Conservative 161; Mismatches 125; Indels
                                                                                      CUDNING: VA

COUNTING: VA

ZTP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: US/08/232,463
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26 AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE COCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF TURENTON: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Alexandria
STREET: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JT 7
US-07-688-352C-31 STANDARD; DNA; UNC; 3073 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/07688352C
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ID US
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Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Wigher, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application PC/TUS9102714

GENERAL INFORMATION:
APPLICANT: Wigher, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Clouding by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 1; Length 3073;
Pred. No. 7.52e-08;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PROOR APPLICATION TABER: US 07/511,715
PILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOLUN, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 25447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TEL
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3.1111
SEQUENCE 3073 BP; 897 A; 684 C; 635 G; 857 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 8
PCT-US91-02714-30 STANDARD; DNA; UNC; 3073 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEY: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID ND: 31:
SEQUENCE CHARACTERISTICS:
LENGIH: 3073 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y march
Local Similarity 88.9%;
tes 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NDCLETC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60603
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Query Match

4.7%; Score 41; DB 3; Length 688;

Best Local Similarity 83.6%; Pred. No. 2.13e-07;

Matches 51; Conservative 0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0AN-1900
Patent No. 5498694.
Patent LO. 5498694.
PAPLICANT: RUOSLAHILERKKI I.
TILLE OF INVENTION: PEPTIDES OF THE CYTOPLASMIC DOMAIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
4.7%; Score 41; DB 2; Length 198;
Best Local Similarity 83.6%; Pred. No. 2.13e-07;
Matches 51; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 688
Sequence 745 BP; 234 A; 132 C; 157 G; 165 T; 57 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 8D4-T3
SEQUENCE 198 BP; 87 A; 20 C; 23 G; 68 T; 0 OTHER.
                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/796,066
FILING DATE: 20-NOVEMBER-1991
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31.503
REFERENCE/DOCKET 31.503
REFERENCE/DOCKET 131.503
REFERENCE/DOCKET 151.227-7400
TELECOMMUNICATION INFORMATION:
TELEFEAX: 617-227-5941
INFORMATION FOR SEQ. ID NO: 16: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,967
FILING DATE: 10-MAY-1994
PRIOR APPLICATION NUMBER: 973,547
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: 357,824
FILING DATE: 25-MAY-1989
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 198 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5498694-3 STANDARD; DNA; UNC; 745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
CELL TYPE: T-cell blast
IMMEDIATE SOURCE:
          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 4.9%; Score 42; DB 2; Length 3073; Best Local Similarity 88.9%; Pred. No. 7.52e-08; Matches 48; Conservative 0; Mismatches 6; Indels
                                                                                                                   COUNTRY: USA

2 IP: 60603

COMPUTER 1 BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR PPPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATPONEY/AGENT INFORMATION:
NAME: BOTUN, MIChael F.
REGISTRATION NUMBER: 25447
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 25447
REFERENCE/DOCKET NUMBER: 2546-556
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 3..1111
SEQUENCE 3073 BP; 897 A; 684 C; 635 G; 857 T; 0 OTHER.
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application PC/TUS9210087
Sequence 16, Application PC/TUS9210087
GENERAL INFORMATION:
APPLICAMT: Smith, Rendall A.
TITLE OF INVENTION: IL-2-Stimulated Gene
TITLE OF INVENTION: Expression
NOMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
ID PCT-US92-10087-16 STANDARD; DNA; UNC; 198 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
COUNTR: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10087
FILING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
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JT 12
PCT-US96-12860-1 STANDARD; DNA; UNC; 2589 BP.
                                     XXXXX
RESULT
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Pred. No. 2.13e-07;
0; Mismatches 19; Indels 0; Gaps
                                                                   Sequence 4, Application US/08361467B

Sequence 4, Application US/08361467B

Rateat No. 56391cation US/08361467B

Rateat No. 56391cation US/08361467B

Rateat No. 56391cation US/08361467B

RAPLICART: Van Emmelo, John
APPLICART: De SOUZA, MATIA: Helena
APPLICART: Van Andreagu, Marc
APPLICART: De SOUZA, MATIA: Helena
APPLICART: Van Andreagu, Marc
TITLE OF INVERTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF INVERTION: BURNIS, DANR, SWECKER & MATHIS
STREET: PO. DAY
ADDING THE STREET PO. DAY
STREET: PO. DAY
ADDING THES: PLOSE DAY
COMPRY: United States
CONTRY: DALES: PLOSE DAY
CONTRY: DALES: PLOSE DAY
CONTRY: DALES: UNIVER: US/08/361,467B
FILING DATE: CALLAND NATA:
APPLICATION NUMBER: US/08/361,467B
FILING DATE: US/08/361,492
FILING DATE: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: 3C9
SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 QTHER.
             T 11
US-08-361-467B-4 STANDARD; DNA; UNC; 1046 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1008 MAAAAAAAAAAAAA 1026
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Local Similarity 75.9%;
les 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                    XXXXX
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Matches
             RESULT
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COUNTAI: USA,
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
SOFTWARE: PATENTEN PCT/US96/12860
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
TELEPROMUNICATION UNMER: A-6444/DJB
TELEPROMUNICATION UNCORMATION:
TELEPROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.7%; Score 41; DB 2; Length 2589;
Best Local Similarity 83.6%; Pred. No. 2.13e-07;
Matches 51; Conservative 0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08199776
Sequence 1, Application US/08199776
Sequence 1, Application US/08199776
Patent No. 5594120
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 5594120el integrin alpha subunit NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
SEQUENCE 2589 BP; 844 A; 436 C; 522 G; 787 T; 0 OTHER.
Sequence 1, Application PC/TUS9612860
Sequence 1, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13

ID US-08-199-776-1 STANDARD; DNA; UNC; 3933 BP.
AC XXXXXX
DE Sequence 1, Application US/0819976
CC APPLICANT: Brenner, Michael B.
CC APPLICANT: Braker, Christina M.
CC APPLICANT: Parker, Christina M.
CC TITLE OF INVENTION: No. 5594120el integrin CC CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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LOCATION: 126..3662
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                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
  COUNTRY: USA
ZIP: 02210
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                                              COMPUTER FELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
FILNG DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISFRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-2441
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: sig_peptide
LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9502044
Sequence 1, Application PC/TUS9502044
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVERTION: Novel integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LI 14
PCT-US95-02044-1 STANDARD; DNA; UNC; 3933 BP.
XXXXXX
                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA HYPOTHERICAL: NO
                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: 180..3659
FEATURE:
                                                                                                                                                                                                                                                                                                              LOCATION: 126.3662
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3907 AAAAAAAAAA 3917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02210
                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
                          STATE: MA
                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                          FEATURE
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COMPITER REMANALE PLOPPY disk
COMPITER: INA COMPATER: PLOPPY disk
COMPITER: INA COMPATER: PLOPPY disk
COMPATER
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NAME/KEY: CDS
LOCATION: 400..4686
OTHER INFORMATION:
SEQUENCE 5108 BP; 1220 A; 1491 C; 1368 G; 1029 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 5108;
Pred. No. 2.13e-07;
0; Mismatches 1; Indels
                 CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
ZUP: 20005
ZUP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
ATOORNEY (AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFFERENCE/DOCKET NUMBER: 1107.033576
TELEFAX: (202) 296-7830
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5108 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CIIY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.7%;
Matches 42; Conservative
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Search completed: Tue Dec 15 19:02:31 1998 Job time: 44 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp Run on:

Tue Dec 15 15:53:21 1998; MasPar time 5.62 Seconds 382.814 Million cell updates/sec

not generated. Tabular output

>US-09-109-864-2 (1-133) from US09109864.pep Title: Description: Perfect Score:

1 MSPRLEVPCSHALPQGLSPG..........LEQLRELRISGSVQLYCVHS 133

PAM 150 Gap 11 Scoring table:

Sequence:

131922 seqs, 16180660 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq32
lipart1 2.part2 3:part3 4:part4 5:part5 6:part6 7:part7
B:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
24:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Mean 30.678; Variance 131.480; scale 0.233 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Pred. No.	2.28e-03	7.19e-01	1.41e+01	2.34e+01	2.34e+01	2.34e+01	2.34e+01	2.34e+01	3.27e+01	4.56e+01	4.56e+01	5.38e+01	5.38e+01	5.38e+01	6.34e+01	6.34e+01	6.34e+01	6.34e+01
	Description	Prostate carcinoma tu	Rat galectin-8.	Ostertagia protective	Protein sequence enco	Human galectin-4-like	Human colon specific	E. coli DNA polymeras	BAV3 ORF6-encoded pro	DNA polymerase III ho	SppR activator protei	Neuronal nicotinic ac	Cdil polypeptide.	Signal transducer and	Signal transducer and	Mac2.16 expression pr	Mac-2 protein includi	Yeast wild-type aceto	Herbicide sensitive,
SUMMARIES	ΙD	W03519	R75702	R72597	W46883	W11841	W06551	W36070	R75761	R40125	W36129	R07143	R54922	W01102	W01101	R12531	R13338	W22458	P81152
	DB	19	13	13	53	23	20	56	13	œ	28	~	10	13	13	m	m	23	-1
	guery Match Length DB	317	316	278	323	323	323	343	983	343	311	495	212	704	748	264	278	687	687
ď	Query Match	14.3	11.1	4.6	9.1	9.1	9.1	9.1	9.1	ø.	8.7	8.7	8.6	8.6	9.0	8.5	8.5	8.5	8.5
	Score	140	109	92	83	83	83	83	83	87	82	82	84	84	84	83	83	83	83
	Result No.	. 4	7	r	4	Ω.	9	7	ω	on	10	11	12	13	14	15	16	17	18

/te recept 6.34e+01	٠.		ы	niveum Cyclosporin 8.79e+01	lipase 1.	ase pr	lipase 1.	ria CO	intracell 1.	5. 1.21e+02	oxidase (P17 1.21e+02	oxidase (wil 1.21e+02	sription f 1.21e+02		ij	2450 homoi 1.42e+02	and placenta le 1.42e+02		sequence 1.42e+02	1.42e+02	pylori transmembra 1.42e+02	ment of m 1.42e+02	protein 1.42e+02	protein- 1.42e+02	nding pr 1	Н
Chicken oocyte recept	Anti-lysozyme VH	IL-4 Stat pe	Yeast transcription	T. niveum Cy	Canine gastric	Dog qastric lipase		Yeast mitoch	Mouse TRADD	Human NF-ATp	ate		Human transcription	Human alpha-	LK26 humanised VH	Cytochrome P450 homol	HL-60 and pl	Human lectin	Amino acid	Human GBP.	H. pylori tr	Peptide fragment of	TATA-binding	TATA-binding	Human TATA-È	RING11 antig
R78233	R43827	R88320	W13826	R44929	R56870	W09382	R56871	W16303	W05530	R60255	R09316	R05793	W0224B	R11749	R82986	R42831	P91964	R08153	R52745	R22625	W20635	R47339	W25017	R56492	W060B3	R25591
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863	123	847	1420	15281	379	379	380	785	227	357	570	570	921	1484	119	125	135	135	135	135	184	195	677	677	677	989
8.5		8	8.3	8.3	8.2	8.2	8 2	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.0	8.0	8.0	8.0	0	8.0		8.0			8.0
83	83	81	81	81	80	80	80	80	79	79	79	79	79	79	78	78	78	78	78	78	78	78	78	78	78	78
19	20	21	22	23	74	25	26	27	28	58	30	31	32	33	34	35	36	37	38	9 9	40	41	42	43	44	45

ALIGNMENTS

The control of the carcinoma tumour antigen and prostate tumour antigen and prostate carcinoma tumour antigen and prostate tumour antigen and calated proteins, vectors, antibodies, etc., for diagnosis and treatment of metastatic cancer.

Disclosure; Fig 18A, 169pp, English.

PCTA (W03519) that is a putative tumour-associated antigen present on prostate cancer cells. Its amino acid sequence was deduced from a cDNA clone (T37414) isolated from human prostatic carcinoma connection and surface epitope masking (SEM) technique. SEM is a method for producing MADS specific for cell surface-expressed molecules. PCTA is a new member of the galectin family, qalectin-8. Antibodies raised against PCTA are useful for the detection of metastatic cancer. Cpds. that inhibit PCTA can be sequence 317 AA; Prostate carcinoma tumour antigen. Prostate carcinoma tumour antigen. Prostate carcinoma tumour antigen. PCTA-1; oncogene; cancer diagnosis; therapy; metastasis; cell surface expression; gurface epitope masking; galectin-8. LT 1
W03519 standard; Protein; 317 AA.
W03519; 11-Jaw-1996; U00307. 11-JaW-1995; US-371377. (UTCO) UNIV COLUMBIA NEW YORK. Fisher PB, Shen R; WPI; 96-342235/34. 26-NOV-1996 (first entry) N-PSDB; T37414 Homo sapiens. WO9621671-A1. 18-JUL-1996 RESULT

Score 140; DB 19; Length 317; Pred. No. 2.28e-03; 41; Mismatches 56; Indels 7; Gaps Query Match
Best Local Similarity 24.6%;
Matches 34; Conservative

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240 vrnsflqeswqeeernitsfpfspgmyfemilycdvrefkvavngvhsleykhrfke-1s 298 : | : ||: :| : | : | : | ద

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AWIS--R--WGQKKLISAPFLFYPQRFFEVLLLFQEGGLKLALNG-QGLGATSMNQQALE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 IS--R--WGQKKLISAPFLEYPQRFFEVLLIFOEGGLKLALNG-QGLGATSKWQQALEQL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hlslpfearinasmgpgrtvvvkgevntnatsfnvdlvagrsrdiaihlnprinvkafvr 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 nsflqdawgeeernitcipissgmyfemiiycdvrefkvavngvhsleykhrfkd-1ssi 299
                                                                                                                                                                                                                                                                                                                                                          Galectin-8 and corresp. DNA - used in regulation of cell growth, esp. inhibition of cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 RLEVPCSHALPQGLSPGQVIIVRGLVLOEPKHFTVSL-RDQAAHAPVTLRASFADRTLAW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                            claim 1; Fig. 1; 44pp; English.

CDNA encoding galactin-8, a novel 35 kDa S-type lectin, was cloned when a lambda ZAP II rat 11ver CDNA library was screened with antibodies directed against the C-terminal end of IRS-1.

Recombinant galectin-8 was expressed in E. coll and CMO cells.

Sequence 316 AA;
                                                                                                                                                                   /note= "N-terminal carbohydrate recognition domain"
                                                                                                                                                                                                                      175..316
/label= CBD
/note= "G-terminal carbohydrate recognition
domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ostertagia protective antigen.
Protective antigen; parasite; immunogen; vaccine; lectin; beta galactoside binding protein.
Ostertagia circumcincta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 109; DB 13; Length 3I Pred. No. 7.19e-01; 41; Mismatches 58; Indels
                                                                                                              Rat galectin-8.
Galectin-8; lectin; antiproliferative; antitumor.
                                                                                                                                                                                                 153..174
/label- Linker_peptide
                                                                                                                                                Location/Qualiflers
                                                                               75702 standard; Protein; 316 AA. R75702;
14-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R72597 standard; Protein; 278 AA.
                                                                                                                                                                                                                                                                                 05-DEC-1994; 013679.
05-DEC-1993; IL-107880.
(RYCU/) RYCUS A.
(YEDA ) YEDA RES & DEV CO LID.
Zick Y;
                    299 sidtleingdihllevrs 316
                                  : | |:| ::| |:|
116 QLRELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.1%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | ::| |:|
118 RELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 dtlavdgdirlldvrs 315
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28-SEP-1993; AU-001494.
(MEAT-) MEAT RES CORP.
                                                                                                                                                                                                                                                                                                                                    WPI; 95-215153/28.
N-PSDB; Q90650.
                                                                                                                                                                                                                                                              W09515175-A
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                                                                                                                                                                                                                                                                         08-JUN-1995
                                                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9509182
                                                                                                                                              Key
domain
                                                                                                                                                                                                 peptide
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                                                                                                                                                                                                                       domain
61
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63 IS-RWG--QKKLISAPFLEYPQRFFEVLLLEQEGGLKLALNGQGLGATSMNQQALEQLRE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 vpyfgrlqggltarrtiiikgyvpptgksfainfkvgssgdialhinprmgngtvvrnsl 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 lngswgseekkithnpfg--pgqffdlsircgldrfkvyangqhlfdfahrlsafqrvdt 309
                                                                                Protective antigens against Ostertagia, Trichostrongylus and Fasciola species — are isolated by a method involving the use of antibody probes from immune, challenged animals
Disclosure; Fig. 55pp. English.
A cDNA library prepared from 3rd stage larvae of O. circumcincta was screened with a Mab raised against a 32-36 'doublet' antigen identified by Western blotting. Clone specificity was determined by plaque immunoassays, and clones were rescued into the plasmid form (pwOSELOX) by plating on E. coll BM25.8 cells. Clones 3-2 and 5-2b contained identical DNA sequences (given in Q86743) encoding a lectin-like beta-galactoside-binding protein (R72597).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim 1; Fig 9; 51pp; English.
W46876-80 and W4682-85 represent proteins encoded by colon-specific genes. The polynucleotides encoding these proteins can be used as probes to detect expression of the corresponding human genes, e.g. in diagnostic assays for detecting micrometastases of colon can Recombinant cells containing the polynucleotides can be used to proteins, in order that antibodies can be raised and used in further screening or diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon-specific nucieic acids - useful as probes for detecting colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSLR-DQAAHAPVTLRASFADRTLAW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-1998 (first entry)
Protein sequence encoded by a colon-specific gene.
Colon-specific gene; probe; detection; expression; human; diagnostic assay; colon cancer; antibody; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 2.34e+01;
36; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB 13; Le
Pred. No. 1.41e+01;
14; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 ipyrskltepfepgqtltvkgktgedsvrftinlhnssa
  Walker
  Newton SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
ID WI1841 standard; Protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 4
W46883 standard, Protein, 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1998.

06-JUN-1995, 469667.

06-JUN-1995; US-469667.

(HUMA-) HUMAN GENOME SCI INC.

MOSEN C. Yu G.

WPI, 98-229823/20.

N-PSDB; V16676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.4%;
Best Local Similarity 28.2%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.1%;
Best Local Similarity 24.8%;
Matches 33; Conservative
Ashman K. Meeusen ENT, WPI; 95-147391/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              278 AA;
                                                           086743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
US5733748-A.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                               W36070 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1994; US-279058.
22-JAN-1993; US-826926.
(CORR ) CORNELL RES FOUND INC.
larity 24.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R75761;
11-NOV-1995 (first entry)
                                                                                                                                                                                                    310 leiggdvtlsyvg 322
                                                                                                                                                                                                                                        120 LRISGSVQLYCVH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-1994; 279058
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference 239
                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
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Matches
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                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: || :||: || | :|:::
63 IS-RWG--OKKLISAPFIFYPQRFFEVILLFQEGGLKLALNGQGLGATSMNQQALEQLRE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 vpyfgrlqggltarrtiiikgyvpptgksfainfkvgssgdialhinprmgngtvvrnsl 251
                                                                                                                                                                                                                                                     Recombinant human galectin 4-like protein and gene - has lactose-binding ability, used in research involving carbohydrate(s) claim 1; Page 13-16; 25pp; Japanese.
Claim 1; Page 13-16; 25pp; Japanese.
This sequence is a human galectin 4 (a lactose-binding protein)-like protein. The protein, which is expressed specifically in the human stomach and intestines, binds lactose and is useful as a drug and as reagent for research involving carbohydrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides (W06545-53) are encoded by cDNA clones (see also T45880-92) corresponding to 13 human colon specific genes, designated CSG1, CSG2, etc., that are primarily expressed in tissues derived from the colon. Recombinant CSG polypeptides can be produced in transformed host celis. They are useful diagnostic markers for colon cancer metastasis and can also be used to screen for colon cancer metastasis and can diagnostic value. Antibodies raised against the colon-specific polypeptides may be used to target colon cancer cells or as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T45888.

Human colon specific genes and their expression products - detect of which, in non-colon tissue samples, can be used as indication colon cancer metastasis
             20-0cT-1997 '(first entry)
Muman galectin-4-like protein.
galectin-4; lactose binding; stomach; intestine; reagent; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon specific gene CSG9 complete polypeptide.
Colon specific gene; CSG9; colon cancer; metastasis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89; DB 23; Length 323
Pred. No. 2.34e+01;
36; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.1%; Score 89; DB 20;
                                                                                                                              30-JAN-1997.
09-JUL-1996; J01899.
11-JUL-1995; JP-174778.
(SAGA ) SAGAMI CHEM RES CENTRE.
Kamata K, Kato S, Sekine S, Yamaguchi T;
WPI; 97-119046/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n 6
W06551 standard; Protein; 323 AA.
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12-DEC-1996.
06-JUN-1995; U07289.
06-JUN-1995; WO-U07289.
ROSEN CA. YU G:
WPI; 97-043054/04.
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.1%;
Best Local Similarity 24.8%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; antibody; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a colon cancer vaccine
                                                                       research; carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 leiggdvtlsyvg 322
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                                                                                                                                                                                                                                    N-PSDB; T59539
                                                                                            HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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16-MAR-1998 (first entry)
E. coli DNA polymerase III delta subunit protein sequence.
Delta subunit; E. coli; DNA polymerase III holoenzyme; probe; enzyme;, hybridisation; PCR.
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N-PSDB; T98154.
Isolated theta, chl. psi, delta and delta' protein sub:units of E. coli polymerase III holo:enzyme - used to make man-made enzyme of 5 or 6 sub:units, useful for long chain PCR Claim 17; Column 11-14; 65pp; English.
This is the amino acid sequence of the delta subunit of the E. coli DNA polymerase III holoenzyme. The gene sequence was isolated from a lambda phage library using probes based on the sequences of the tryptic peptides W36072-W36075.
The E. coli polymerase III subunits (theta, chi, psi, delta and delta' (T98151-T98155 respectively) are used to make man-made enzymes comprising 5 or 6 subunits and potentially for use in long chain PCR.
                                                                                                       192 vpyfgrlqggltarrtiiikgyvpptgksfainfkvgssgdialhinprmgngtvvrnsl 251
                                                                                                                                                                                                                                                252 lngswgseekkithnpfg--pgqffdlsircgldrfkvyangqhlfdfahrlsafgrvdt 309
                                                                                                                                                                                                                                                                                     :: || :||: || | |::::
63 IS-RWG--QKKLISAPFLEYPQNEFEVLLLFQEGGLKLALNGQGLGATSMNQQALEQLRE 119
                                                                                                                                                                      7 VPCSHALPQGLSPGQVIIVRGLVLQEPKMFTVSLR-DQAAHAPVTLRASFADRTLAW--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 hilqqlrlggsepvillrtl-qrel-lllvnlkrqsahtp--lralf-dkhrvwgnrrg 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
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                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAV3 ORF6-encoded protein.
BAV3; vector; vaccine; gene therapy; fiber protein.
Bovine adenovirus type 3.
Pred. No. 2.34e+01;
36; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99. 101
/label= N-glycosylation_site
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/label= N-glycosylation_site
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6

SOUCH STANDARD STANDA

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4 RLEVPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSLRDOAAHAPVTLRASFADRTLAWI 63
                                                                                                                                                                                                                                                           231 hllqqlrlegsepvillrtl-qrel-lllvnlkrqsahtp--lralf-dkhrvwqnrrg 284
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This protein is the encoded product of the Streptomyces snpR activator gene. The snpR activator gene is incorporated in novel plasmid pawr195 (see V01451) that also includes the SnpR-activated snpA promoter and a modified doxA gene (see V01447) of Streptomyces sp. strain C5. The doxA gene codes for daunomycin C-14 hydroxylase (see W36128), an enzyme capable of converting daunomycin to the anticancer agent doxcubicin. Host cells, especially Streptomyces host cells, transformed with pawr195 can be used in methods for the production of doxcrubicin from daunomycin or for the hydroxylation and oxidation of other
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                 Producing doxorubicin from daunomycin by daunomycin C14 hydroxylase also hydroxylation and oxidation of other anthracycline(s) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SnpR activator protein.
Daunomycin C-14 hydroxylase; doxA gene; doxorubicin; daunomycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-dihydrocarminomycin; carminomycin; anthracycline; anticancer; cytostatic; cancer; therapy; plasmid pANT195; SnpR. Streptomyces sp.
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Pred. No. 4.56e+01;
14; Mlsmatches 22; Indels
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Neuronal nicotinic acetylcholine receptor beta 4 subunlt.
Rat; nAChR.
                                                                                                                  DB 8; Length 343;
                                                                                                                                                                                      Indels
                                                                                                              Score 87; DB 8; Lence Pred. No. 3.27e+01; 13; Mlsmatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..20
/label-signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OHIS ) UNIV OHIO STATE RES FOUND.
DeSanti CL, Dickens ML, Strohl WA;
WPI: 98-018495/02.
N PSDB: V01451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W36129 standard; Protein; 311 AA. W36129;
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R07143 standard; protein; 495 AA
                                                                                                          Query Match 8.9%;
Best Local Similarity 39.0%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
   delta subunit hola gene.
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22-MAY-1997, U08690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anthracyclines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SRW 66
                                         Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine adenovirus expression vector system - comprising insertion of required genes into deletions in El and E3 and transformation of mammalian cell lines, useful in vaccines and gene therapy Disclosure; Fig.7H-R; 159pp; English.

BAV3 strain WBR-1 genomic DNA, from between 77 and 92 m.u., was cloned into plasmids and sequenced. ORFs that had the potential to encode polypeptides of at least 50 amino acids (R75756-61) were identified. The amino acid sequence at the N-terminus of the ORF6-encoded protein shared approx. 60% identity with the HAd2 fiber protein tall, but there was little similarity in the knob region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 16-17; 115pp; English.
The sequence is that encoded by the DNA polymerase III holoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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Pred. No. 2.34e+01;
12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1994 (first entry)
DNA polymerase III holoenzyme delta subunit holA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 ltfengavrakl-gpglgtddsgrsvvrtgrglrvangqvgif 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | |::|::: | | |||: | | ||: | ||:: | ||:: | ||:: | ||:: | ||:: | ||:: | ||:: | ||:: | ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: 
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09-DEC-1993; US-164292.
(UYSA-) UNIV SASKATCHEWAN.
Babluk LA, Graham FL, Mittal SK, Prevec L; WPI: 95-224330/29.
N-PSDB; 090769.
                                                                                                                                                                                                                                                   74.576
label N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                             819..821 //label= N-glycosylation_site 847..849
                                                                                                  68..270
label- H-glycosylation_site
                                                                                                                                                                           426..428
/label= N-glycosylation_site
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label- N-glycosylation_site
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Tabel N-glycosylation_site
53.855
Tabel N-glycosylation_site
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/label= N-glycosylation_site
913..915
/label N-glycosylation_site
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R40125 standard; Protein; 343 AA.
R40125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1993.
22-JAN-1993; U00627.
24-JAN-1992; US-826926.
(CORR) CORNELL RES FOUND INC.
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Best Local Similarity 32.6%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI, 93-258618/32.
N-PSDB; Q47197.
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DNA encoding human signal transducer and activator of transcription of traetment of e.g. neoplasia traetment of e.g. neoplasia traetment of e.g. neoplasia traetment of e.g. neoplasia claim 1; Pagee 25; 32pp; English.

Claim 1; Pagee 25; 32pp; English.

Human signal transducer and activator of transcription 4-beta (Stat4-beta) (WD102) is an interleukin-12 signal transducer conceptor subunit. Its amino acid sequence was deduced from a cDNA receptor subunit. Its amino acid sequence was deduced from a cDNA clone (T38325) isolated from human peripheral blood lymphocytes. A cliferent isoform, Stat4-alpha (W01101), is the product of a cDNA clone (T38325) obtd. from Junkat cells. Recombinant Stat4 proteins can be produced in transformed host cells. They find use in screening assays for cpds. useful in the diagnosis, prognosis or treatment of diseases associated with undestrable cell growth, differentiation and/or cytokine signal responsiveness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 ltvgssysdghltw-akfckehlpgksftfwt-wleaildlikkhilplwidgyvmgfvs 579
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The sequence is that of a protein, Cdil, which complexes with Cdc2 family proteins. It is expressed during G1 to S transition and may negatively requiate the passage of cells through this part of the cycle, thus linking the requiatory networks connecting extracellular signals with core cell cycle controls. Cdil may function to remove cells from active cycle to allow differentiation, and there are cancers in which lesions in the G1 requiatory machinary prevent cdil from exherting its full effect. The protein was isolated using the novel bait-trap method described in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal transducer and activator of transcription 4-beta. Signal transducer and activator of transcription 4; Stat4; interleukin-12; signal transduction; neoplasm; cancer; diagnosis;
                                                                                                                               Determining whether protein interacts with known protein, esp. with Cdc2 - useful to detect cancer and to develop anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
8.6%; Score 84; DB 19; Length 704;
Best Local Similarity 23.8%; Pred. No. 5.388+01.
Matches 19; Conservative 27; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 8.6%; Score 84; DB 10; Length 212; Local Similarity 45.8%; Pred. No. 5.38e+01; es 11; Conservative 7; Mismatches 6; Indels
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27; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 lsdtispeqaidslrdlrgsgaig 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 13
W01102 standard; Protein; 704 AA.
                                     Gyuris J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 MNQQALEQLRELRISGSVQL 128
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(GEHO ) GEN HOSPITAL CORP.
Brent R, Golemis E, Gyun
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22-MAR-1996; U03868.
22-MAR-1995; US-408318.
(TULA-) TULARIK INC.
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WPI; 96-443132/44.
                                                          WPI; 94-167458/20.
N-PSDB; 065494.
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Matches
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Thera 4 sub-unit and DNA sequences encoding them.

Sclaim 8; Fig 3; 47pp; English.

The sequence, of a novel neuronal nicotinic acetylcholine.

The sequence, of a novel neuronal nicotinic acetylcholine.

The sequence, of a novel neuronal nicotinic acetylcholine.

Control of the sequence of a novel neuronal nicotinic acetylcholine.

Control of the sequence of a novel nicotinic acetylcholine.

Control of the sequence of the sequence of the september of the known subunits. Alpha-2.-3, and -4, and beta-2 to form previously unknown functional receptors. The new subunit is expressed in subunits, alpha-2.-3, and -4, and beta-2 to form previously unknown functional receptors. The new subunit is expressed in the as the characteristics of a ligand-gated ion channel subunit, including four transmembrane domains. The cystein residues like and the Torpedo electric organ alpha subinit are present at posns. 152 and 166. The beta 4 subunit is distinctive in having four rather than two glycosylation sites. Of the three organical beta-type subunits, beta 4 has the logest cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Cdc2: Gl stage: Gl - S transition: regulator: differentiation;
cancer: interaction trap system.
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Pred. No. 4.56e+01;
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Hellemann SF; Deneris ES; Duvoisin RM; Patrick JW; 90-304987/40.
N-PSDB; Q06068.
                                                                                                                                                                 'note="membrane spanning region""
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                                                                                                                                                                                                                                                                                                                                                                  'note="membrane spanning region"
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                        21..495
/label=nAChR beta 4 subunit
237..256
/label=MSR I
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Tabel-N-glycos_site
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Tabel-N-glycos_site
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Tabel-N-glycos_site
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R54922;
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/label-MSR III
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/label-MSR IV
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Best Local Similarity 31.9%;
Matches 15; Conservative
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12-MAR-1990; US-492555.
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20-OCT-1993; U10069.
30-OCT-1992; US-969038.
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cleavage_site
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WO9410300-A.
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The encoding human signal transducer and activator of transcription to the encoding human signal transducer and activator of transcription to treatment of e.g. neoplasia claim 1; Page 21-23; 32pp; English.

Claim 21; Page 21-23; 32pp; Page 21-23; 32pp; Page 21-23; 32pp; Page 21-23; 32pp; Page 21-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 ltvqssysdghltw-akfckehlpgksftfwt-wleaildlikkhilplwidgyvmgfvs 579
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                                                                                                                                                       Signal transducer and activator of transcription 4-alpha. Signal transducer and activator of transcription 4; Stat4; interleukin-12; signal transduction; neoplasm; cancer; diagnosis;
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Clone Mac2.16 was isolated from a lambda gtl1-P388D1 expression
library prepared from activated mouse macrophages. This is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84; DB 19; Length 748;
Pred. No. 5.38e+01;
27; Mismatches 30; Indels
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HMEBP; leishmaniasis; Nouse Mac-2; laminin.
T 14
W01101 standard; Protein; 748 AA.
W01101;
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R12531 standard; Protein; 264 AA.
R12531;
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29-NOV-1990; U06948.
30-NOV-1989; US-444195.
14-SEP-1990; US-582628.
(GEHO-) GEN HOSPITAL CORP.
Pillal S. Cherayll BJ;
WPI: 91-193196/25.
N-PSDE; Q12207.
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Best Local Similarity 23.8%;
Matches 19; Conservative
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                                                                                                                 03-JAN-1997 (first entry)
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22-MAR-1996, U03868.
22-MAR-1995, US-408318.
(TULA-) TULARIK INC.
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WO9108290-A.
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195 wg-keerqsafpfesgkpfkiqvlveadhfkvavndahllqynhrmknlreisqlgisgd 253
                                                                                                                                                                                                                 Score 83; DB 3; Length 264;
Pred. No. 6.34e+01;
15; Nismatches 30; Indels 1; Gaps
          ť
deduced amino acid sequence of the Mac2.16 expression product. I has predicted mol. wt. 27,482. The N-terminal domain contains a repetitive Proline/Glycine-rich motif and the C-terminal domain contains a sequence found in S-type lectins. See also Q12208-Q12111.
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                                                                                                                             8.5%;
Local Similarity 27.0%;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Run on:

Tue Dec 15 15:56:27 1998; MasPar time 2.20 Seconds 427.387 Million cell updates/sec

Tabular output not generated.

>US-09-109-864-2
(1-133) from US09109864.pep
980
1 MSPRLEVPCSHALPQGLSPG.....LEQLRELRISGSVQLYCVHS 133 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

77309 segs, 7078906 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Mean 28.678; Variance 129.097; scale 0.222 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P						
Score		Query	Length	EG.	ឧ	Descr	g	pred. No.
8		9.1	323	. 2	PCT-US95-0	Sequence 1	16, Applicati	1.07e+01
8		9.1	323	Н	US-08-469-	Sequence 1	6. Applicati	1.07e+01
æ	_	6	343	Н	US-08-279-	Sequence		1.07e+01
à		80.0	212	Н	US-08-461-	Sequence	5. Applicati	2.43e+01
æ	4	9.	748	Н	us-08-839-		2. Applicatio	2.43e+01
à	-	80.00	748	Н	US-08-408-			2.43e+01
æ	н	æ.	847	⊣	US-08-781-	Sequence	2, Applicatio	3.94e+01
80	a	89.3	847	Н	US-08-276-	Sequence 2	2, Applicatio	3.94e+01
	0	8.5	785	Н	US-08-526-	Sequence 4	1, Applicatio	4.62e+01
7	6	8.1	227	⊣	US-08-414-	Sequence 4	1, Applicatio	5.42e+01
7	6	8.	357	~	PCT-US94-0	Sequence 1	2. Applicati	5.42e+01
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7	φ	8.1	921	-4	US-08-396-	Sequence 2	, Applicatio	5.42e+01
7	σ.	80	921	Н	US-08-818-	Sequence 2	2, Applicatio	5.42e+01
7	00	8.0	119	\leftarrow	US-08-207-		20, Applicati	6.35e+01
7	00	80.0	125	Н	US-08-313-		54, Applicati	6.35e+01
~	28	80.0	195	(4	PCT-US93-0	Sequence 5	9, Applicatio	6.35e+01
7	00	8.0	195	Н	us-08-063-	Sednence 5	, Applicatio	6.35e+01
7	00	8.0	677	Н	US-08-646-	Sequence 1	13, Applicati	6.35e+01
7	.	8.0	677	Н	US-08-188-	Sequence 1	13, Applicati	6.35e+01
~	~	7.9	312	Н	US-08-414-	Sequence	3, Applicatio	7.44e+01
<u>۱</u> -	~	7.9	708	Ä	-767-70-SD	Sequence 2	2, Applicatio	7.44e+01
,		7.9	708	Н	ns-08-308-	Sequence 2	2, Applicatio	7.44e+01

7.7 7.9 708 2 PCT-US95-0 Sequence 2, Applicatio 7.44e+01 7.9 708 1 US-08-162 Sequence 5, Applicatio 7.44e+01 US-08-476 Sequence 25, Applicati 8.70e+01 105-08-476 Sequence 25, Applicati 8.70e+01 105-08-08-65 Sequence 25, Applicati 8.70e+01 105-08-08-08-08-08-08-08-08-08-08-08-08-08-	ALIGNMENTS	5-07289-16 STANDARD; PRI; 323 AA.		e 16, Application PC/TUS9507289	equence 16, Application PC/TUS9507289 GENERAL INFORMATION: APPLICANT: Yu, Guo-Liang APPLICANT: Yu, Guo-Liang APPLICANT: Rosen, Craig TITLE OF INFUNITON: Colon Specific Genes and Proteins NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSEE: Caralla, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Garalta, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Garalta, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Garant & Olstein CITY: Roseland STREET: 6 Becker Farm Road CITY: Roseland STREET: 6 Becker Farm Road COUNTRY: USA ZIP: 07068-1799 COMPUTER: IBM FC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 COMPUTER: BatentIn Release #1.0, Version #1.30 COMPUTER: Depart POT/VS95/07289 FILING DATE: 06-JUN-1995 CLASSIFICATION NUMBER: 90-T/VS95/07289 FILING DATE: 06-JUN-1995 CLASSIFICATION NUMBER: 3128800-265 TELEPOMUNICATION NUMBER: 3128800-265 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION TOR SEQ ID NO: 16: SEQUENCE CHRACATERISTICS: LENGTH: 323 amino acid TYPE: amino acid TYPE: amino acid MOLECULE TYPE: protein
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                                                                                               192 VPYFGRLQGGLTARRTIIIKGYVPPTGKSFAINFKVGSSGDIALHINPRMGNGTVVRNSL 251
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                                                       Gaps
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                                                                                                                                                                                                                                                                               Sequence 16, Application US/08469667
Patent No. 5733748
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
Score 89; DB 2; Length 323;
Pred. No. 1.07e+01;
36; Mismatches 55; Indels
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                                                                                                                                                                                              323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FETFATO, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-435
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 323 AA; 35941 MW; 553806 CN;
                                                                                                                                                                                                                                                             Sequence 16, Application US/08469667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
IYPE: amino acids
                                                                                                                                                                                               STANDARD;
Query Match 9.1%;
Best Local Similarity 24.8%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6 Becker
CITY: Roseland
STATE: NJ
                                                                                                                             310 LEIQGDVTLSYVQ 322
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US-08-469-667-16
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Pred. No. 1.07e+01:
14: Mismatches 15; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 HILQQLRLGGSEPVILLRTL-OREL-LLLVNLKRQSAHTP--LRALF-DKHRVWQNRRG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 HALPQ-GLSPGQ-VIIVRGLVLQEPKHFTVSLRDQAAHAPVTLRASFADRTLAWISRWG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICALLON.

PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
RRGISTRATION NUMBER: 26,824
RREFERENCE/DOCKET NUMBER: CRF D-1056CIP
TELECOMMUNICATION INFORMATION:
TTLECOMMUNICATION INFORMATION:
                  343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥
                                                                                                                                                    Sequence 9, Application US/08279058B
Patent No. 5668004
GENERAL IMPORMATION:
APPLICANT: Michael E. O'Donneil
TITLE OF INVENTION: HOLGENZME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: MICROSOft Word 4.0
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/279,058B
                  PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE 343 AA; 38674 MW: 551136 CN;
                                                                                                                             Sequence 9, Application US/08279058B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08461859
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 343 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (203)268-1951
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.1%;
Best Local Similarity 39.0%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
JT 3
US-08-279-058B-9
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                                                        XXXXXX
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US-09-109-864-2.rai

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522 LIVOSSYSDGHLIW-AKFCKEHLPGKSFIFWI-WLEAILDLIKKHILPLWIDGYVMGFVS 579
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Patent No. 5639658
GENERAL INFORMATION:
APPLICANT: Hoey, Timothy
ATILE OF INVENTION: Human Signal Transducers and Binding
TITLE OF INVENTION: Assays
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herber
STREET: 850 Hansen Way, #200
          CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herber STREET: 850 Hansen Way, #200
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%; Score 84; DB 1; Length 748; Best Local Similarity 23.8%; Pred. No. 2.43e+01; Matches 19; Conservative 27; Mismatches 30; Indels
                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 748 AA; 85940 MW; 3117180 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08408318
                                                                                                                                                                                                                                                                                                                   NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8700
TELEFAX: 415-494-8771
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-494-8771
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         : 748 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 MNQDALEQLRELRISGSVQL 128
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NUMBER OF SEQUENCES:
                                                                                        USA
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COUNTRY: USA
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US-08-408-318-2
                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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       Sequence 35, Application US/08461859
Patent No. 5786169
Patent No. 5786169
GENERAL INFORMATION:
APPLICANT: GULTIS, Jeno
APPLICANT: GOLEMIS, Telca
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5786169e1 Proteins
NUMBER OF EQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STREET: Assachusetts
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Patent No. 5756700
GENERAL INFORMATION:
APPLICANT: Howey, Timothy
TITLE OF INVENTION: Human Signal Transducers and Binding
TITLE OF INVENTION: Assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 8.6%; Score 84; DB 1; Length 212; Local Similarity 45.8%; Pred. No. 2.43e+01; Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                            STATE: MASSACIUSELUS
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM;
EDDIUM TYPE: 3.5" DISKETTE, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETTE, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordferfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,859
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Raien F.
REGISTRATION NUMBER: 35,238
REFERENCE/POCKET NUMBER: 07/86/143002
TELEPRAN: (617) 542-5070
TELEPRAN: (617) 542-5070
TELEPRAN: (617) 542-5070
TELEPRAN: (617) 542-8906
TELES NUMBER: SEG ID NO: 35:
SEQUENCE CHARACIENISTICS:
SEQUENCE CHARACIENISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 212 AA; 23806 MW; 219064 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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104 LGATSMNQQALEQLRELRISGSVQ 127
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Matches
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US-09-109-864-2, rai

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515 W-QWFDGVLDL 524
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                                                                                                                                                                                                                                                                                   27; Mismatches 30; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08781890
Patent No. 5710266
GENERAL INFORMATION:
APPLICANT: MCKLight, Steven L
APPLICANT: MCKLight, Steven L
APPLICANT: MCKLight, Steven L
APPLICANT: MOUNTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND TITLE OF INVENTION: INTERCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STARE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,890
FILING DATE: 05-JAN-1997
CLASSIFICATION NUMBER: US-08/276,099
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard Aron
                                                                                                                                                                                                                           Query Match

8.6%; Score 84; DB 1; Length 748;
Best Local Similarity 23.8%; Pred. No. 2.43e+01;
Matches 19; Conservative 27; Mismatches 30: Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,318
                                                                                                                                                                                                                                                                                                                                                                          847 AA
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 748 AA; 85940 MW; 3117180 CN;
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                 FILING DATE:

CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: OSMAIN. RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-606
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8771
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LINGTH: 748-amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08781890
                                                                                                                                                                                                                                                                                                              580 KEKERL-LLKD-KMPGTFLL 597
                                                                                                                                                                                                                                                                                                                         109 MNQQALEQLRELRISGSVQL 128
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                                                                                                                                                                                                         SEQUENCE
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REFERENCE/DOCKET BURGER: A-59451-1/RaO
TELEPRONE/DOCKET BURGER: A-59451-1/RaO
TELEPRONE/DOCKET BURGER: A-59451-1/RaO
TELEPRONE/CATION TREPRATION:
TELEPRONE (413) 783-1369
TOPOLOGY: linear
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Matches

XXXXXX

RESULT

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APPLICANT: Goeddel, David V.
APPLICANT: Hsu, Hailing
TITLE OF INVENTION: INTRACELLULAR SIGNALING PROTEINS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, NOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compartible
OPERATIOS SYETEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
PILLICATION NUMBER: US/08/414,625
FILLIG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LOAYREGALRTALQ-RCM-APALAQEALRLQL-ELR-AGAEQL 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                           E: FLEHR, NOHBACH, TEST, ALBRITT
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET JODG/
REFERENCE/DOCKET NUMBER: A-60916/RAO
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 494-8701
TELETAX: (415) 494-8771
TELEX: 910 277999
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
                                                                                        227
      1 MSPRLEVPCSHALPQGLSPGQV-IIVRGLVLQEPKH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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GENERAL INFORMATION:
APPLICANT: Rao, Anjana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOLECULE TYPE: protein
JENCE 227 AA, 25323 MW, 222467 CN;
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application PC/TUS9400545
                                                                                                                                                                                                                                                      Sequence 4, Application US/08414625
Patent No. 5563039
GENERAL INFORMATION:
                                                                                                                                                                                                                Sequence 4, Application US/08414625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 227 amino acids
amino acid
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTR: USA
ZIP: 94111-4187
CONPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.1%;
Best Local Similarity 41.9%;
Natches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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                                                                  US-08-414-625-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                   XXXXXX
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                                                                  RESULT
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                                                                                                                                               461 AEVGTURGL-L--PENF-LFLAQKIFNDNSLSM-EAFQNRSVSW-SQFNKEILLGRGFTF 514
                                                                                                                                                                         20 GQVIIVRGLVLQEPKHFTVSLRDQA-AHAPVTLRASFADRTLAWISRWGQKKLISAPPLF 78
                                                                                                         8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lambowitz, Alan N
APPLICANT: Lambowitz, Alan N
APPLICANT: Lambowitz, Ateven
APPLICANT: Zimmerly, Steven
APPLICANT: Guo, Nucleotide Integrase Preparation
APPLICANT: Vang, Jian
TITLE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Nalter & Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                         # Match 8.3%; Score 81; DB 1; Length 847; Local Similarity 29.6%; Pred. No. 3.94e+01; hes 21; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.2%; Score 80; DB 1; Length 785; Best Local Similarity 33.3%; Pred. No. 4.62e+01; Matches 12; Conservative 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 MA-RLTNSCKECLGFSLIPSHLGIVINAYVLEEEVN 114
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MOLECULE TYPE: protein
SEQUENCE 847 AA; 94134 MW; 3802900 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08526964
Patent No. 5698421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET UNDER: 2272
TELECOMMUNICATION INFORMATION:
TELEFAM: (216) 622-8200
TELEFAM: (216) 241-0816
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 785 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08526964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLLICK, MAIY E
REGISTRATION NUMBER: 34,829
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
NOLECULE TYPE: peptide
HYPOTNETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                 515 W-OWFDGVLDL 524
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79 YPQRFFEVLLL 89
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US-08-526-964-4
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Patent No. 5612455
GENERAL INFORMATION:
APPLICANT: HOEY, Timothy
TITLE OF INVENTION: NDCLEAR FACTORS AND BINDING ASSAY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: ADDRESSE: FLEHR, ROBBACH, TEST, ALBRITTON & HERBERT
STREET: A Embarcadero Center. Suite 3400
CITY: San Francisco
STARE: California
CONTYRY: DSA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: NEW PC COMPATIBLE
COMPUTER: READABLE FORM:
MEDIUM TYPE: RIPP PC COMPATIBLE
COMPUTER: READABLE FORM:
COMPUTER: READABLE FOR
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                                                                                                STATE: MASSACIMSELLE
COUNTRY: U.S.A.
ZIP: 0.210-2804
COMPUTER READABLE FORM
EDIDM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145.006C
FILING DATE: October 29, 1993
CLASSIFICATION NUMBER: 08/01/052
APPLICATION NUMBER: 08/01/052
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: January 12, 1993
ATTONEY/ACENT INFORMATION:
NAME: FRASE, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 04590/007001
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-8906
TELERAX: (617) 542-8906
TELERAX: (617) 542-8906
TELERAX: 200154
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 82
                        E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
SEQUENCE 357 AA; 37623 WW; 700002 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08396479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                     CITY: Boston
STATE: Massachusetts
      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-396-479B-2
                          ADDRESSEE: 2:
STREET: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08145006C
Patent No. 5656452
GENERAL INFORMATION:
APPLICANT: Reo, Anjana
APPLICANT: Hogan. Patrick Gerald
APPLICANT: McCaffrey, Patricia
APPLICANT: Jain, Jugun
TTLE OF INVENTION: NF-ATP, A T LYMPHOCYTE
TITLE OF INVENTION: DNA-BINDING PROTEIN
NUMBER OF SEQUENCES: 21
APPLICANT: Hogan, Patrick Gerald
APPLICANT: McCaffrey, Patricla
APPLICANT: Jain, Jugar
APPLICANT: Jain, Jugar
TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE
TITLE OF INVENTION: DNA-BINDING PROTEIN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 AA
                                                                                                                                                                   51 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 82
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| MSPRLEVPCSHALPQGLSPGOVIIVRGLVLQEP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOGY: linear
357 AA; 37623 MW; 700002 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08145006C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPRACE (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 357
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ID DS-08-145-006C-12
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                                                                                                                                                Length 921;
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8.0%; Score 78; DB 1; Length 119;
Best Local Similarity 28.3%; Pred. No. 6.35e+01;
Matches . 15; Conservative 17; Mismatches 17; Indels
                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: Miled States of America
APPLICANT: Now York, New York 10105
APPLICANT: Now York, New York 10105
APPLICANT: United States of Americas
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                            119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
                                                                                                                                                Score 79; DB 1; L
Pred. No. 5.42e+01;
12; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATTICLA A.
REGISTATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                              109 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 140
                                                                                                                                                                                                                                                                         :|||:||: || || ||:::| ||:::|
1 MSPRLEVPCSHALPQGLSPGQVIIVRGLVLQEP 33
LENGTH: 921 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
SEQUENCE 921 AA; 99784 MW; 4492223 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
FENCE 119 AA; 12852 MW; 80291 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08207996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-838-388
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                              Query Match 8.1%;
Best Local Similarity 36.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM IYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                       US-08-207-996-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXX
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Patent No. 5708158
GENERAL INFORMATION:
APPLICANT: HOEY, Timothy
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
NUMBER OF SEQUENCES: 18
CORRESPONDENE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA
CONTER: CALIFORNIA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,823
FILING DATE: 14-MAR-1997
CLASSIFICATION NUMBER: 08/396,479
FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHAID A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/CONCET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                          FILLE CALLS

TIMESTEL CANDON

NAME: Osman. Richard A

RECISTRATION NUMBER: 36.627

REFERENCE/DOCKET NUMBER: A-59450-1/RAO

TELECHONE: (415) 494-8771

TELERAX: (415) 494-8771

TELEX: 210 277299

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 921 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         921 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.1%; Score 79; DB 1; La
Best Local Similarity 36.4%; Pred. No. 5.42e+01;
Matches 12; Conservative 12; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 140
  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/396,479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSPRLEVPCSHALPQGLSPGQVIIVRGLVLQEP 33
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 921 AA; 99784 MW; 4492223 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08818823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 14
US-08-818-823-2
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67 RVTMLRDTSKNOFSLRLSSVTAADTAIYICARHGDDP-AWFAYWGGGSLVTVS 118 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... g

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在我我我我们的人,我们的人,我们们的人,我们们的人,我们们的人,我们们们的人,我们们们的人,我们们的人,我们们们的人,我们们的人,我们们们的人,我们们们们们的人,	<u> </u>	· · · · · · · · · · · · · · · · · · ·

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 15 15:54:30 1998; MasPar time 7.48 Seconds 606.724 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-109-864-2 (1-133) from DS09109864.pep 980 1 MSPRLEVPCSHALPOGLSPG.......LEQLRELRISGSVQLYCVHS 133 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

107076 segs, 34141958 residues Searched:

Minimum Match 08 Listing first 45 summaries Post-processing:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 42.737; Variance 90.659; scale 0.471 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	7.78e-12	1.19e-06	4.56e-06	9.92e-03	2.46e-02	2.46e-02	6.03e-02	4.60e-01	6.11e-01	1.41e+00	1.41e+00	2.45e+00	2.45e+00	3.22e+00	3.22e+00	4.21e+00	5.50e+00	5.50e+00	5.50e+00	7.18e+00	7.18e+00	7.18e+00	9.34e+00
Description	galectin-5 - rat	prostate carcinoma tu	galectin-7 - human	ų	qalectin-8 - rat	lactose-binding lecti	UDP-N-acetylglucosami	14K beta-galactoside-	nosF protein - Pseudo	enterobactin receptor	sodium channel protei	probable general secr	sodium channel protei	complement factor 1 (glutathione-regulated	ATP-binding cassette	galactoside-binding p	tance	pqqF protein - Klebsi	global nitrogen regul	hypothetical 87.1K pr	(B)	_
ឧ	A55932	JC6147	155469	A42846	A55975	A46631	A27522	LNCH14	S13584	A40636	A60165	A65126	JC1101	A29154	OOECRD	B41538	A49800	A64101	520458	A48640	J01866	S57964	B40361
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ouery Match	17.8	14.3	13.9	11.4	11.1	11.1	10.8	10.1	10.0	9.7	9.7	9.5	9.5	4.6	9.4	9.3	9.3	9.2	9.2	9.1	9.1	9.1	9.0
Score	174	140	136	112	109	109	106	66 .	86	95	95	66	93	92	92	91	90	06	06	88	68	68	80
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A40347	VCBVBV	A36024	A45251	F69109	B69172	H64817	RNRZC2	RNZMB2	S71628	S75654	S52256	S22561	B69058	A54909	S07792	B35721	A48528	JC1300	A45391	A47704	JC4037
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Surface-epitope masking and expression cloning identifies the human prostate carcinoma tumor antigen gene PCIA-1 a member of the galectin gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This protein is a therapeutic reagent for intervention in pervasive and fatal neoplastic disease. It is involved in an earlier genetic change in human prostate cancer development. This protein is a member of the genectin familly.
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J. Blol. Chem. (1995) 270:5823-5829
Cloning, expression, and chromosome mapping of human
                   240 VRNSFLQESWGEEERNITSFPFSPGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKE-LS 298
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#formal_name Homo sapiens #common_name man
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Su, Z.Z.; Lin, J.; Shen, R.; Fisher, P.E.; Goldstein,
Fisher, P.B.
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A42846 #type complete
beta-galactoside-binding protein GBP - Caenorhabditis elegans
beta-galactoside-binding lectin homolog, 32K
#formal_name Caenorhabditis elegans
10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
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J. Biol. Chem. (1992) 267:15485-15490
Evidence that Caenorhabditis elegans 32-kDa
beta-galactoside-binding protein is homologous to
vertebrate beta-galactoside-binding lectins. cDNA cloning
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                                                                                                                                                                   63 NSKEQGSWGREERGPGVPFQR-GQPF-EVLIIASDDGFK-AVVGDAQYBHFRHRLPLARV 119
                                                                                                                                                                                             3 NVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVF 62
                                                                                                          6 EVPCSHALPQGLSPGQVIIVRGLVLQEPKHFIVSL---RDQAAHAPVILRASFADRTLAW 62
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galectin-8 - rat
#formal_name Rattus norvegicus #common_name Norway rat
23.Mar-1995 #sequence_revision 05-Apr-1995 #text_change
10-Sep-1997
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Galectin-8. A new rat lectin, related to galectin-4.
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                                           39; Mismatches 47; Indels 11;
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Pred. No. 2.46e-02;
41; Mismatches 58; Indels
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Pred. No. 9.92e-03;
12; Mismatches 13;
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Score 136; DB 2;
Pred. No. 4.56e-06;
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Best Local Similarity 35.9%;
Matches 14; Conservative
Query Match 13.9%;
Best Local Similarity 28.1%;
Matches 38; Conservative
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Best Local Similarity 22.1%;
Matches 30; Conservative
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118 RELRISGSVQLYCVH 132
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J. Biol. Chem. (1993) 268:5929-5939
Soluble Lactose-binding lectin from rat intestine with two different carbohydrate-binding domains in the same peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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Purification and characterization of the N-terminal domain galectin-4 from rat small intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-RWGQKKLISAPF-LFYPQRFFEVLLLFQEGGLKLALNGQGLGATSMNQQALEQLRELR 121
181 MLSIPFEARLNASMGPGRTVVVKGEVNTNATSFNVDLVAGRSRDIALHINPRLNVKAFVR 240
                                                               NSFLQDAWGEEERNITCFPFSSGMYFEMIIYCDVREFKVAVNGVMSLEYKMRFKD-LSSI 299
                                                                                  194 VPYVGTLØGGLTARRIIIKGYVLPTAKNLIINFKVGSTGDIAFHMNPRIGDCVVRNSYM 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 NGSWGSEE-RKIPYNPFGAGQFFDLSIRCGTDRFRVFANGQHLFDFSMRFQAFQRVDMLE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence extracted from NCBI backbone (NCBIN:128409, NCBIP:128410)
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21.5ep-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998
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protein YBR1628; protein YBR243c
protein Zacharomyces cerevisiae
15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
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                  A27522 #type complete
UDP-N-acetylglucosamine--dolichyl-phosphate
N-acetylglucosaminephosphotransferase (EC 2.7.8.15)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status preliminary
##molecule_type nucleic acid
##residues 1-324 ##label ODA
##cross-references GB:M73553; NID:9294571; PID:9294572
###experimental_source intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type protein
##residues 13-37;44-50,'E',52-66 ##label TAR
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                                                                                                                                                                                                                                             lactose-binding lectin L-36 - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                           chain.
#cross-references MUID:93194902
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                                                                                                                              300 DILAVDGDIRLLDVRS 315
                                                                                                                                                            118 RELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                               galectin-4
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13-Mar-1998
A27522; 546120
$ERENCE A27522
#authors Martog, K.O.; Bishop, B.
#journal Nucleic Acids Res. (1987) 15:3627
#fittle Genomic sequence coding for tunycamicin resistance in yeast.
#accession A27522
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                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references EMBL: 236112; NID: 9536652; PID: 9536653; MIPS: YBR243c
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TW7/
TW8/
TW9/
TW10/
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Hirabayashi, J.; Kawasaki, H.; Suzuki, K.; Kasai, K.I.
J. Biochem (1987) 101:775-783
Complete amino acid sequence of 14 kDa
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#length 448 #molecular-weight 50367 #checksum 4659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 106; DB 2; Length 448
Pred. No. 6.03e-02;
21; Mismatches 32; Indels
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14% beta-galactoside binding lectin - chicken
14% lectin
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predicted
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#domain transmembrane *status
#domain transmembrane *status
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J. Biochem. (1988) 104:173-177
                                                                                                                                                                                                                                                                                                                                                                   1-448 ##label ALJ
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Best Local Similarity 24.7%;
Matches 19; Conservative
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KEYWORDS
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80K - Pseudomonas aeruginosa

#titie

2-135

SUMMARY

FEATURE

GENETICS

REFERENCE

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#authors Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.
#journal Nucleic Acids Res. (1987) 15:8569-8572
#title Nucleotide sequence of the putative sodium channel gene from brosophila: the four homologous domains.
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sodium channel protein - fruit fly (Drosophila melanogaster)
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#title Genomic organization and deduced amino acid sequence of a putative sodium channel gene in Drosophila.
#cross-references MID:87292090
#accession A60165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##status preliminary
##molecule_type nucleic acid
##residues 1-746 ##label DEA
##cross-references GB:M98033; NID:g151434; PID:g151435
##note extracted from NCBI backbone (NCBIN:122308,
##note
                                                                                                                                                                                                                                                                                    #authors Dean, C.R.; Poole, K.
#journal J. Bacteriol. (1993) 175:317-324
#title Cloning and characterization of the ferric enterobactin receptor gene (pfeA) of Pseudomonas aeruginosa.
#cross-references MUID:93123148
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22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
16-Feb-1997
                                                                        enterobactin receptor protein, 80K - Pseudomonas aerugir
#formal_name Pseudomonas aeruginosa
21-5ep-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1994
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trons 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1;
751/2; 801/1; 908/1; 960/3; 1005/1
ir #length 1321 #checksum 3413
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Pred. No. 1.41e+00;
10; Mismatches 12; Indels
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##residues 1-362;363-626;627-1321 ##label SAL
##cross-references EMBL:X14394
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#length 746 #molecular-weight 80967 #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 FTVSLRDQAAHAPVTLRASFA-DRTLAWISRWGOKKL 71
                                               #tyPe complete
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Best Local Similarity 37.8%;
Matches 14; Conservative
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#journal Bur. J. Blochem. (1990) 192:591-559
#title Nitrous oxide reductase from denttrifying Pseudomonas
stutzeri. Genes for copper-processing and properties of the
deduced products, including a new member of the family of
#Cross-references WUID:91006150
                                                                                                                                                                                                                   Ohyama, Y.; Hirabayashi, J.; Oda, Y.; Ohno, S.; Kawasaki, H.;
Suzuki, K.; Kasai, K.
Blochem. Biophys. Res. Commun. (1986) 134:51-56
Nucleotide sequence of chick 14K beta-galactoside-binding
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th 308 #mclecular-weight 33777 #checksum 7279
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beta-galactoside-binding lectin of chick embryo. #cross-references MUID:87250364
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Pred. No. 4.60e-01;
15; Mismatches 16; Indels
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acetylated amino end; lectin
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                                                                                                         ##molecule_type protein
##residues 2-110,112-135 ##label HIR
ENCE A24062
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*cross-references MUID:86130505
*accession A24062
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##cross-references GB:AE000409; GB:U00096; NID:g1789718; pID:g1789723;
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Biochem. Biophys. Res. Commun. (1992) 186:61-68
Primary structure of sguid sodium channel deduced from the
                                                                                                                                                   sodium channel protein - Bleeker's squid
#formal_name Loligo bleekeri #common_name Bleeker's squid
09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
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#formal_name Escherichia coli
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#cross-references WUID:97426617
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Pred. No. 2.45e+00;
15; Mismatches 28; Indels
 Pred. No. 1.41e+00;
13; Mismatches 14; Indels
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                                                736 SLRTLRALRPLRAISRWQGMRIVVNALMYAIPSIFNVLLV 775
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#cross-references MUID:92337659
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Matches 22; Conservative
Best Local Similarity 32.5%;
Matches 13; Conservative
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PEBS Lett. (1995) 371:199-203
beta-Sheet secondary structure of an LDL receptor domain
complement factor I by consensus structure predictions
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#title Human complement factor I: analysis of cDNA-derived pristrocture and assignment of its gene to chromosome 4.
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##residues 1-557,'F',559-583 ##label GOL
##cross-references GB:J02770; NID:g182606; pID:g182607
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Characterization of the primary amino
complement control protein factor I
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##residues 1-583 ##label CAT
##cross-references GB:Y00318
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#crossreferences MUID:87241401
#accession A29154
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35.0%;
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14; Conservative
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##molecule_type protein
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##experimental_source strain K12 NCE A64720

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#journal Nucleic Acids Res. (1980) 8:2255-2274
#ifile Nucleotide sequence of the Escherichia coli gene coding for dihydrofolate reductase.
#cross-references NUID:81053692
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##cross-references EMBL:D10483; NID:g216434; PID:d1001795; PID:g216472
                                                                                                                                                                                                                                                                                                                                           *domain signal sequence *status predicted *label SIG\
*product complement factor I heavy chain *status
predicted *label CFH\
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glutathione-regulated potassium efflux system protein kefc
Escherichia coli
                                                                                                                                                                                         *superfamily LDL receptor ligand-binding repeat homology;
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05-Apr-1983 #sequence_revision 01-Mar-1996 #text_change
14-Nov-1997
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Mol. Microbiol. (1991) 5:607-616
The Cloning and DNA sequence of the gene for the glutathione-regulated potassium-efflux system RefC Escherichia coll.
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#length 583 *molecular-weight 65720 *checksum 3015
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Pred. No. 3.22e+00;
3; Mismatches 7; Indels
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##residues 1-620 ##label MUN
##cross references EMBL:X36742; NID:g41874; PID:g41875
SNCE A93704 ..... T M
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glycoprotein; hydrolase; serine proteinase
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                                                                                                  ##cross_references GDB:120077; OMIM:217030
#map_position 4q24-4q25
CLASSIFICATION #superfamily LDL receptor linand
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##molecule_type_DNA
##molecule_type_DNA
500-620 ##label_SMI
258-269 ##label ULI
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#accession S15165
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Best Local Similarity 52.4%;
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Job time : 23 secs.

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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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#domain transmembrane #status predicted #label TM4\
#domain transmembrane #status predicted #label TM4\
#domain transmembrane #status predicted #label TM5\
#domain transmembrane #status predicted #label TM5\
#length 620 #molecular-weight 67795 #checksum 3086
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                                                                                                                              Fjournal Science (1997) 277:1453-1462
*title The complete genome sequence of Escherichia coli K-12.
*cross-references_MUD:97426617
                                                                                                                                                                                                                                                   preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 3.22e+00;
19; Mismatches 27; Indels 10;
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Best Local Similarity 34.9%;
Matches 30; Conservative
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CLASSIFICATION #super
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Tue Dec 15 15:55:45 1998; MasPar time 10.89 Seconds 608.412 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

>US-09-109-864-2 (1-133) from US09109864.pep 980 Title: Description: Perfect Score: Sequence:

1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133

PAM 150 Gap 11 Scoring table:

165420 seqs, 49795644 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb16 Database:

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 42.859; Variance 78.955; scale 0.543 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

5	Description		QI .	QI .	DB ID	Query Match Length DB ID
ដ	36 KD BETA-GALACTOSIDE GALACTOSIDE	O35866 36 KD B	., .	., .	354 11 035866	354 11 035866
ż	GALECTIN-7			11 054974	11 054974	11.5 136 11 054974
œ.	W09H1.6B	_	_	5 045904	285 5 045904	11.4 285 5 045904
Ŀ	GALECTIN-3	_	_	13 090713	262 13 090713	11.3 262 13 090713
•	GALECTIN-6	O54891 GALECTIN		11 054891 (301 11 054891	11.3 301 11 054891
	GALECTIN.	O44126 GALECTIN	_	_	283 5 044126	11.2 283 5 044126
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μ,	BETA-A PROTEIN.		14 Q83076	14 Q83076	195 14 Q83076	10.2 195 14 Q83076
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4	COMPLEMENT COMPONENT		11 Q61129	11 Q61129	603 11 Q61129	603 11 Q61129
г	REVERSE TRANSCRIPTASE	O64428 REVERSE	10 064428	10 064428	1309 10 064428	1309 10 064428
	PUTATIVE INNER MEMBRAN	O70110 PUTATIVE	2 070110	2 070110	295 2 070110	295 2 070110
	ABC-TRANSPORTER.	Q28438 ABC-TRANS	6 028438	6 028438	6 028438	6 028438
	SODIUM CHANNEL PROTEIN	_	5 027930		5 027930	5 027930
	GALECTIN		5 001411	5 001411	5 001411	5 278 5 001411
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6.88e+00	CONSERVED PROTEIN.	027843	Н,	346	6.8	87	36
6.88e+00	COAT PROTEIN.	089433 065721	14	198		84	
5.11e+00	HETICAL 32	005769	N	295		88	33
5.11e+00	32.4 KD	P93740	10	291	0	88	32
3.79e+00	LIPOXYGENASE (EC 1.13.		10	862	9.1	88	30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TPQLRLPFAARLNTPMGPGRTVVVKGEVNANAKSFNVDLLAGKSKDIALHLNPRLNIKAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 VRNSFLOESWGEEERNITSFPFSPGMYFEMITYCDVREFKVAVNGVHSLEYKHRFKE-LS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 KWGREERGTGIPFQR-GOPF-EVLLIATEEGFK-AVVGDD-EYLHFHHRLPPARVRLVEV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 SLPQGVRVGTVMRIRGLVPDQAGRFHVNLLCGEEQGADAALHFNPRLDTSEVVFNTKQQG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SPRLEVPCSHALPQGLSPGQVIIVRGLVLOEPKHFTVSL-RDQAAHAPVTLRASFADRTL
                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALECTIN-7.
MUS MUSCULUS (MOUSE).
EUKRAKOTA, METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           f Match 11.5%; Score 113; DB 11; Length 136; Local Similarity 27.7%; Pred. No. 1.46e-03; nes 36; Conservative 37; Mismatches 44; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 141; DB 4; Length 318; Pred. No. 4.56e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C59 BLACKC/6;
MAGNALDO T., FOWLLS D., DARMON M.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BENEL; AF018562; G2708654;
PROSITE: PS00309; LECTIN_GALACTOSIDE; 1.
SEQUENCE 136 AA; 15173 MW; 61A0164B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-BRAIN HIPPOCAMPUS;
HADARI Y.R., ETSENSTEIN M., ZAKUT R., ZICK Y.;
TRENDS GLYCOSCI. GLYCOSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CS9 BLACKC/6;
MEDLINE; 95246905.
MAGHALDO I., BERNERD F., DARWOH M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEV. BIOL. 168:259-271(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | |:| ::| 1:|
116 QLRELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 24.6%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 SIDTLEIHGDIHLLEVRS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054974;
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGDVQLHSLN 134
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GALECTIN-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JT 3
054974
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Matches
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셤
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SEQUENCE FROM N.A.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
A BUTLSON R., CONNELL M., COPERT T., COUCER J., COULSON A., CRAXTON M.,
BURTON J., CONNELL M., COPERT T., TOOPER J., COULSON A., CRAXTON M.,
A BURTON J., LAISTER R., FATELLO R., JONES M., KERSHAW J.,
A KIRSTEN J., LAISTER H., LATREILLO P., LIGHNING J., LLOYD C.,
A MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., LOYD C.,
A RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
SONNHAMMER E., STADEH R., SULSTON J., THTERRY MIEG J., THOMAS K.,
A WILKINSON-SPROAT J., WOHLDMAN P.,
IN NATURE 368 32-38 (1994).
IR EMBL; 282081; E1247370; ..
REMBL; 282081; E1247370; ..
REMBL; 282081; E1247370; ..
REMBL; 282081; E1247370; ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALLUS GALLUS (CHICKEN).
EUKRRYOTA; METAŽOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGHATHAE;
GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TL-AMI--SRWGOKKLISAPFLFYPORFFEVILLFOEGGLKLALNGOGLGATSMYQOALE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 IVCNSMFQNNWGNEBRTAPREPGTPFKLQYLCEGDHPRYAVNDAHLLQPNFREKKLN 24.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AAPLKVPYDLPLPAGLMPRLLITITGTVNSNPNRFSLDFRRGODIAFHFNPRFKEDHKRV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SPRLEVPCSHALPQGLSPGQVIIVRGLVLQEPRHFTVSL-RDQA-A-HAPVTLRASFADR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                     SUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                     SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                      06, CREATED)
06, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATIOH UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSLRDQAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 VPYRSVLQEKFEPGQTLIVKGSTIDESQRFTINLHSKTA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 112; DB 5; Pred. No. 2.07e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LECTIN.
SEQUENCE 262 AA; 28155 NW; FD6F1E17 CRC32;
                            285 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
TISSUB-CARTILAGE,
NURMINSKAYA M.V., LINSENWAYER T.F.;
DEV. DRV. 0.0-0(0).
EMBL: US0339; G1389600; -.
PFAM: PF00337; Gal-bind_lectin.
                            PRT;
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07;
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Best Local Similarity 25.0%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 35.9%;
Matches 14; Conservative
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                       PRELIMIHARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMIHARY;
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01-NOV-1996 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                  01-JUN-1998 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
                                                                           (TREMBLREL.
                                                                                                                                                                           CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                        01-JUN-1998
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LT 4
045904
045904;
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090713;
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LT 8
Q20684
Q20684;
Q1-NOV-1996
01-NOV-1996 (
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                                                                                                                                                                                                                                                                                                                                                                                                                             231 NGSWGTEERMVAYN-PFGPGQFFDLSTRCGMDRFKVFANGIHLFNFSHRFQALRKINTLE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAL-1.
HAEMONCHUS CONTORTUS.
EUKARYOTA: METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA,
EUTBERIA, RODENTIA.
                                                                                                                                                                                                                                                 GITT M.A., XIA Y.R., ATCHISON R.E., LUSIS A.J., BARONDES S.H.,
LEFFLER H.;
                                                                                                                                                                                                                                                                                                                                                                    ;
6
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                                                                                                                                                                                                                                                                                                                                               Length 301;
                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-129/6V;
GTTT M.A., COLNOT C., POIRIER F., NANI K.J., BARONDES S.H.
LEFFILER H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110; DB 5; Length 283;
Pred. No. 4.14e-03;
12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEWLANDS G.F.J., SKUCE P.J.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF036098; G.2687413; -..
SEQUENCE 283 AA, 32530 NW; 9EAE3746 CRC32;
                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                             Score 111; DB 11; I
Pred. No. 2.93e-03;
36; Mismatches 56;
                                                                                                                                                                                                                                                                      J. BIOL. CHEM. 273:2961-2970(1998).
EMBL; AF026799; G2914749; --
EMBL; AF026796; G2914749; JOINED.
EMBL; AF026797; G2914749; JOINED.
EMBL; AF026798; G2914749; JOINED.
EMBL; AF026798; G3914749; JOINED.
                                                 301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 AA
                                                                     CREATED)
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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044126 PRELIMINARY;
044126 01-JUN-1998 (TREMBLREL. 06, CR
01-JUN-1998 (TREMBLREL. 06, LA
01-AUG-1998 (TREMBLREL. 07, LA
                                                                    06,
06,
                                                                                                                                                                                                                                                                                                                                              Match 11.3%;
Local Similarity 25.2%;
Hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.2%;
Best Local Similarity 35.9%;
Matches 14; Conservative
                                                                                                                                                                                                   J. BIOL. CHEM. 0:0-0(1997).
: | |:| : | |
116 QLRELRISGSVQLYCV 131
                                                 PRELIMINARY;
                                                                  01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 INGDLTLSYVH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| : | ||
122 ISGSVQLYCVH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-MOREDUN;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 STRAIN=129/SV;
MEDLINE; 98112848.
                                                                                                  GALECTIN-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALECTIN.
                                                                                                                                                                                                                                                                                                                                              Query Match
                                     LT 6
054891
054891;
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Matches
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THE SEQUENCE FROM N.A.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
WILSON R., AINSCOUGH R., COPERT J., CONDER J., CONDEIL M., COPERT J., COLLEGON A., CRANTON M.,
RA BURKINS T., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDDER R., GREEN P.,
RA HAWKINS T., HILLER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
MCWUTRAY A., MORTIMORE B., SAUNDERS D., SHOWNKEEN R., SNALDON N., SMITH A.,
SONNHAMMER E., STADEN R., WATERSTON J., THIERRY-MIEG J., THOMAS R.,
NAULINSON-SPROAT J., WOHLDMAN P.;
NAILKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(1994).

BR EMBL; Z66512; G1041326; --
DR EMBL; Z66512; G1041326; --
DR PFAM; PFO0337; G31-bind_lectin.

SCOUENCE 1262 AA; 133688 MW; 96ECBD5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1132 VPYESGLAGEGLAPGKTLTVFGIPEKKAKRFHINLLKKNGDIALHLNARFDEKHVVRNS 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITTDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 102; DB 5; Length 280;
Pred. No. 6.19e-02;
15; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      GARDNER A.; SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-UDN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
BETA-CAACTOCSIDE-BINDING LECTIN.
ONCHOCERCA VOLVULUS.
                                                                                                                                                                                               01, CREATED)
01, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches 25;
                       Score 104; DB 5;
Pred. No. 3.18e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VPYRSKLTESFEPGQTLLVKGKTAEDSVRFTINLHNTSA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 AA; 31978 MW; FC532581 CRC32;
15 VPYRSLLOEKIEPGOTLIVKGSTIDESQRFTINLHSKSA
                                                                                                                                                   1262 A.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLION A.D., DONELSON J.E.;
MOL. BIOCHEM. PARASITOL. 65:305-315(1994).
EMBL; U04046; G433317; -.
PFAM; PF00337; Gal-bind_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.4%;
llarity 30.8%;
Conservative
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ilarity 27.1%;
Conservative
                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                               1-NOV-1996 (TREMBLREL.
1-NOV-1996 (TREMBLREL.
1-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                      CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity (
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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064428
064428;
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061129
      SORESPERSORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PLPQGVRLGTVMRIRGVVPDOAGRFHVNLLCGEEQEADAALHFNPRLDTSEVVFNTKQQG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYCHNIS RINGSPOT VIRUS.
VIRIDAE: SS-RNA NONENVELOPED VIRUSES: ROD-SHAPED SS-RNA VIRUSES;
MORDEIVIRUS.
                                                                                                                                                    RAITUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA: TETRAPODA: MAMMALIA:
EUIHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.3%: Score 101: DB 11; Length 132:
Best Local Similarity 25.8%: Pred. No. 8.61e-02;
Matches 33; Conservative 34; Mismatches 50: Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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01-546-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-546-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-546-1998 (TREMBLREL. 07, LAST ANNOTALION UPDAIE)
TERPENE CYCLASE LIKE PROTEIN.
F1C12.120.
F1C12.120.
FARBINDOSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; PLANTA, EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 PSNALVARDVQPLRDSALHFTYDLKDLVTSDPPVFDRRSFEAKFOLNWVAR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 10.2%; Score 100; DB 14: Length 195; Best Local Similarity 31.4%; Pred. No. 1.19e-01: Matches 16; Conservative 14; Mismatches 17; Indels
                                                                                                                                                                                                                                                              STRAIN-FISHER;
MAGNALDO T., DARMON M.:
SUBMITTED (C-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF035641; G2587659; -.
PROSITE; PS00309; LECTIN_GALACIOSIDE: 1.
SEQUENCE 132 AA; 14889 MW; 9BBBGC4D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLOYYEV A.G.:
SUBMITTED (OCT-1994) TO EMBL/GENBANK/DDBJ DAIA BANKS.
EMBL; 246351; E122444; -..
SEQUENCE 195 AA; 21709 MW; 04D0D3B9 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAIE)
                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                        132 AA
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                                                                   CREATED)
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                        PRT;
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083076;
083076;
01-NOV-1996 (TREMBLREL. 01, CF
01-NOV-1996 (TREMBLREL. 01, LP
01-NOV-1998 (TREMBLREL. 01, LP
BETA-A PROTEIN.
OLT 10
054958 PRELIMINARY;
034950
01-JUN-1998 (TREMBLREL. 06, LJ
01-JUN-1998 (TREMBLREL. 06, LJ
01-AUG-1998 (TREMBLREL. 07, LJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                  GALECTIN-7
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065434
065434:
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MOL. IMMUNOL. 33:101-112(1996).
MOL. IMMUNOL. 33:101-112(1996).
MOL. IMMUNOL. 33:101-112(1996).
PROSITE: R0105937; CFI.
PROSITE: R0105937; LDLRA_1; 1.
PROMIN: PROMOUS; LIMITECEPt_A.
PRAM: PROMOS; LYPPSIN.
PROMOS; LYPPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 KDFILEEALSFTSSMLESLAASGTCPPHLSVRIRNALGLSQHWNMEMLVPVEFIPFYEQE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 RGLVLQEPKHFTVS-LRDQAAHAPVTLRASFADR-TLAWISRWGQKKLISAPFL-FYPQR 82
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                                               BEVAN M., TERRYN N., ARDILES W., BUYSSHAERT C., DASSEVILLE R., DE CLERCK R., DE KEYSER A., MEYT P., ROUZE P., VAN DEN DAELE H., VILLAROCEL R., GIELEN J., VAN MONTAGU M., BANCROFT I., MEWES H.W. MAYER K., SCHUELLER C.; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHOKDATA: VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                Length 573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVERSE THANSCRIPTASE.
CHORRELA VULGARLS.
EUKARVIA. PLANTA; CHLOROPHYTA (GREEN ALGAE):
CHLOROPHYCEAE: CHLOROCOCCALES; OCCYSTACEAE.
                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.0%: Score 98; DB 10: Length 573
Best Local Similarity 28.2%: Pred. No. 2.28e-01;
Matches 22; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                                                                       EU ARABIDOPSIS SEQUENCING PROJECT:
SUBMITIED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; ALO22224; E1283969; -- SEQUENCE 573 AA; 66617 MW: 21B69D3A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      051129;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-UON-1996 (TREMBLREL. 06. LAST ANNOTATION UPDATE)
COMPLEMENT COMPONENT FACTOR I (COMPLEMENT FACTOR I)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 RWGEVDLIGNCSOFYPDRYYE 525
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07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.0%;
Best Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 F-FEVILL-FQEGGLKLA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE)
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE; 96175003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                        Gaps
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                                                                                             Score 97; DB 10; Length 1309;
Pred. No. 3.15e-01;
15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.8%; Score 96; DB 2; Length 295;
Best Local Similarity 36.1%; Pred. No. 4.33e-01;
Matches 26; Conservative 14; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
OCER P. M. V. VAUDEQUIN-DRANSART V., DESSAUX Y.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF065542; G3153870; -.
EMBL; U67851; G3033355; -.
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CHRYS;
OGER P.M., VAUDEQUIN V., DESSAUX Y.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
SEQUENCE FROM N.A.
TRANSPOSON-ZEPP;
HIGASHIYAMA T., NOUTOSHI Y., FUJIE M., YAMADA T.;
EMBO J. 16:371373(1997).
EMBL; AB008896, D1026697; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1309 AA; 141659 NW; C874E321 CRC32;
                                                                                                                                            810 KHLGIPLSTOPAAATALYTAIIEKVEARIARWSGFRL 847
                                                                                                                                                         SEQUENCE 295 AA; 32054 MW; DD8DEF72 CRC32;
                                                                                              Query Match
9.9%,
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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